

FIG.1

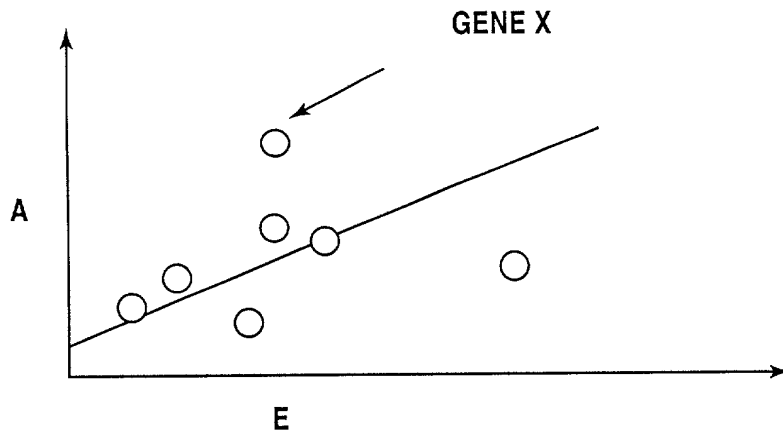


FIG.2

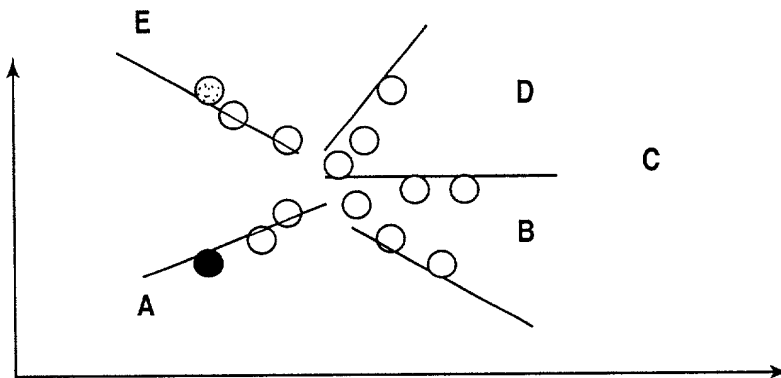


FIG.3

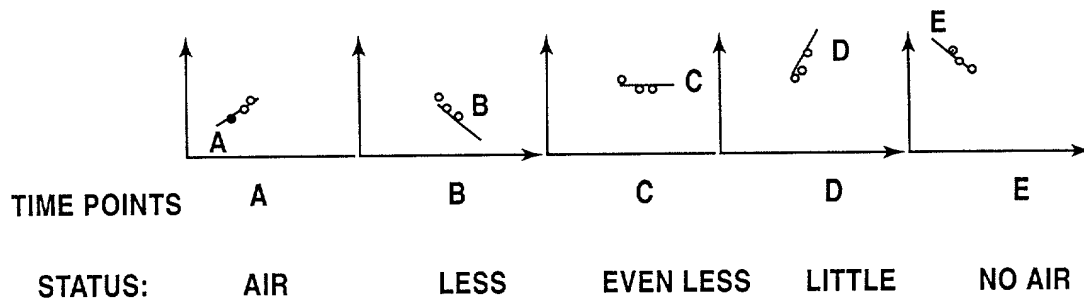



FIG.4

Please, log in



array SCOUT™

Login

lion

Password

Account

lion

OK

Cancel

Fig.5

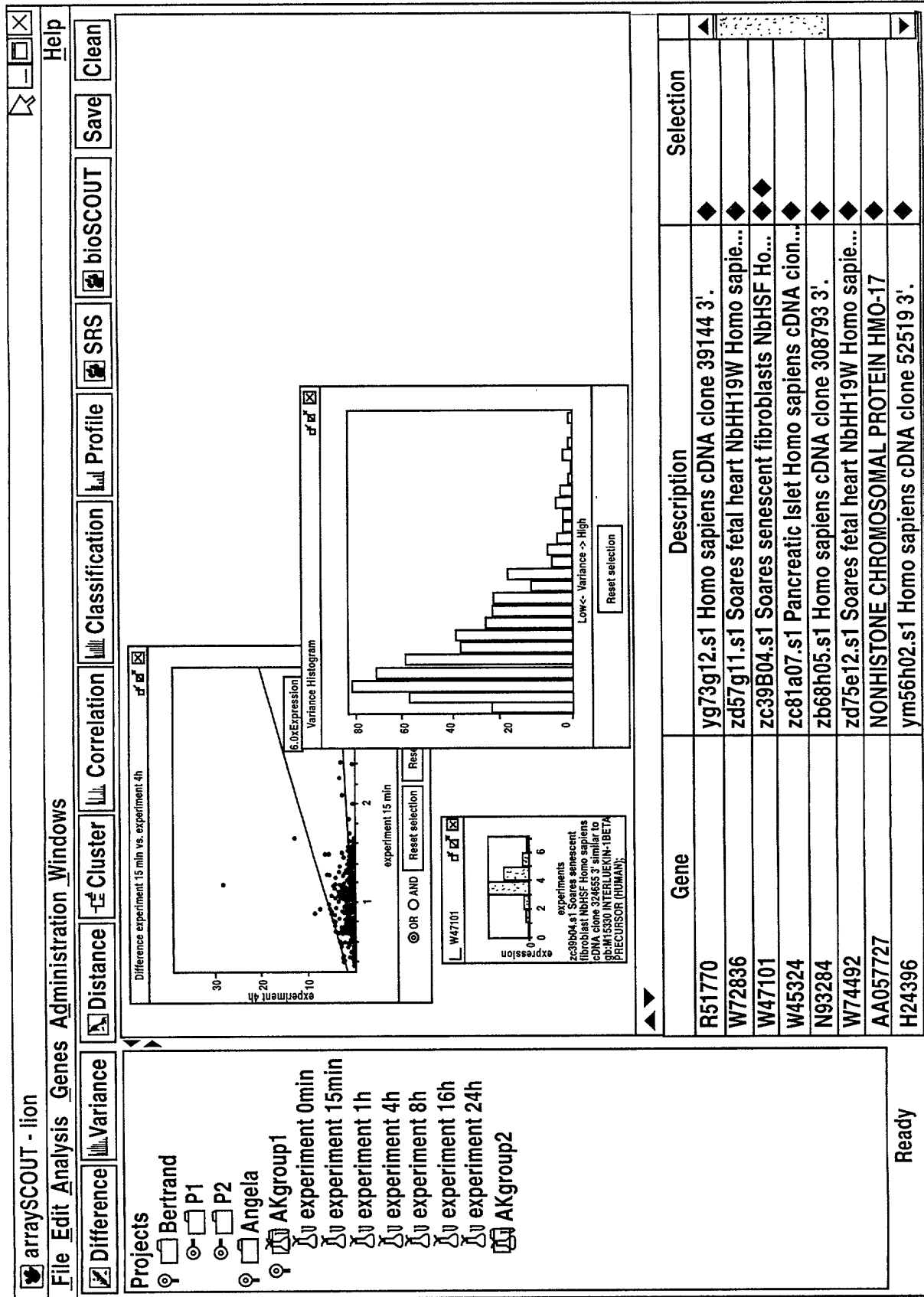


Fig.6

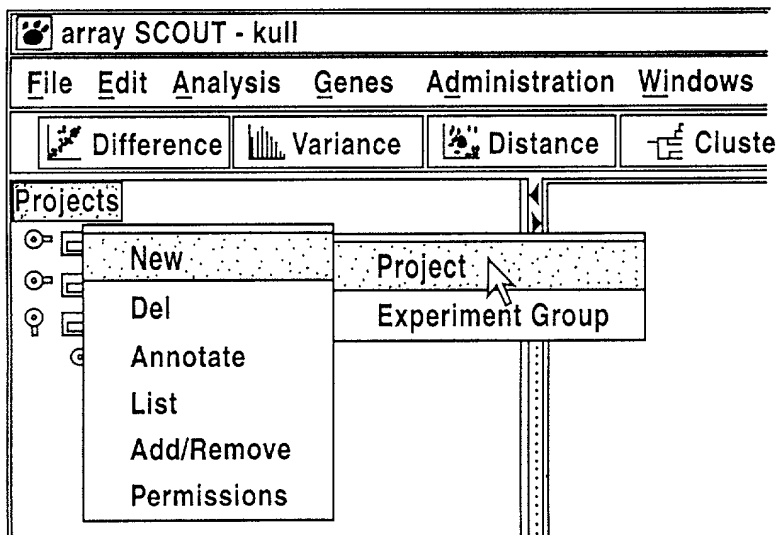


Fig.7

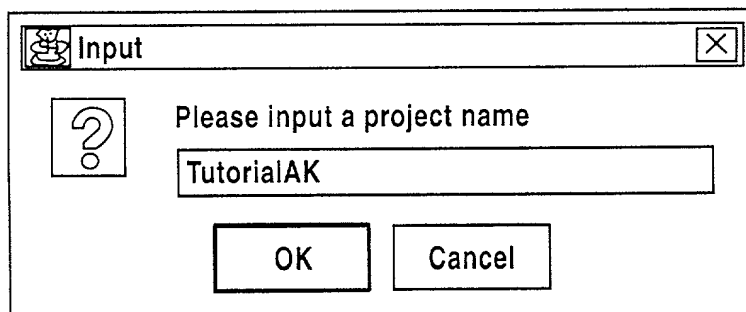


Fig.8

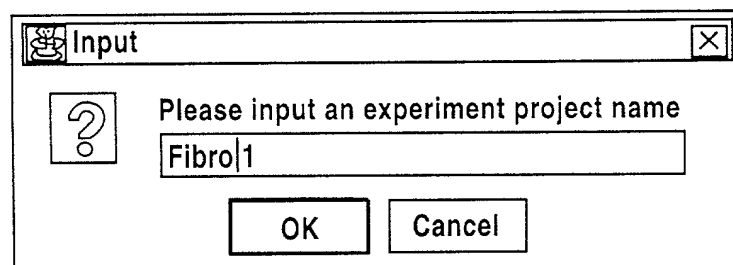


Fig.9

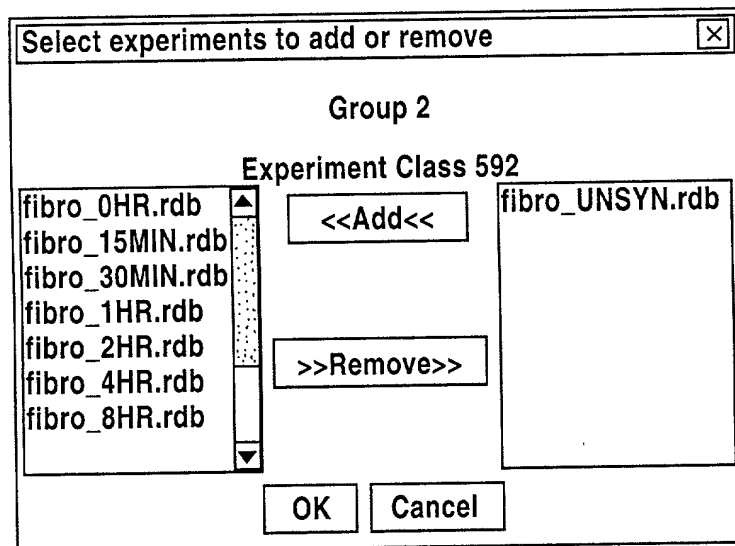


Fig.10

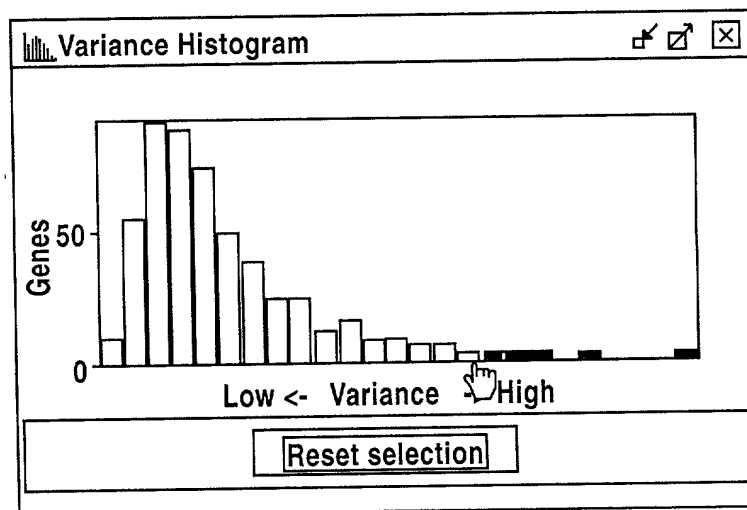


Fig.11

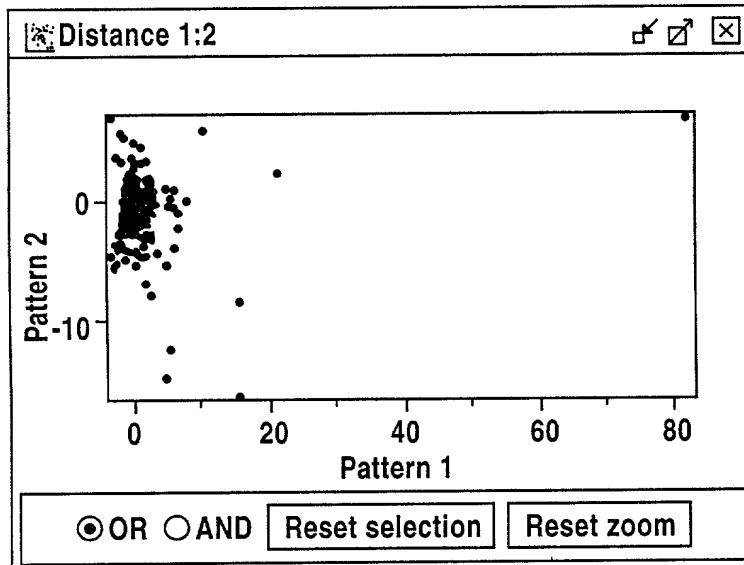


Fig.12

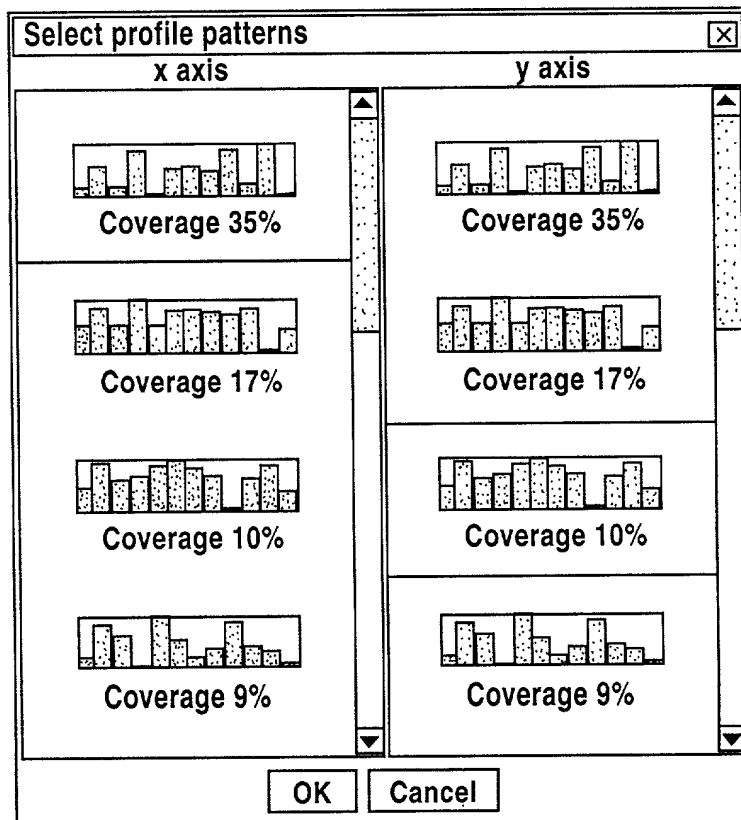


Fig.13

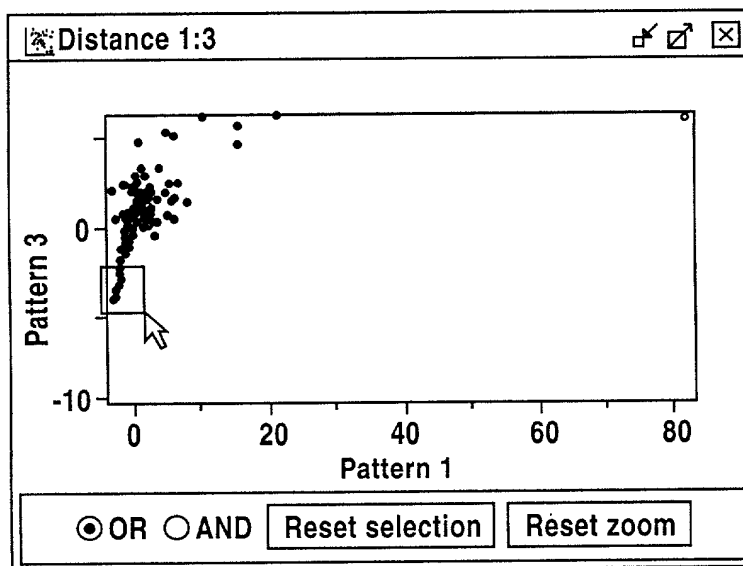


Fig.15

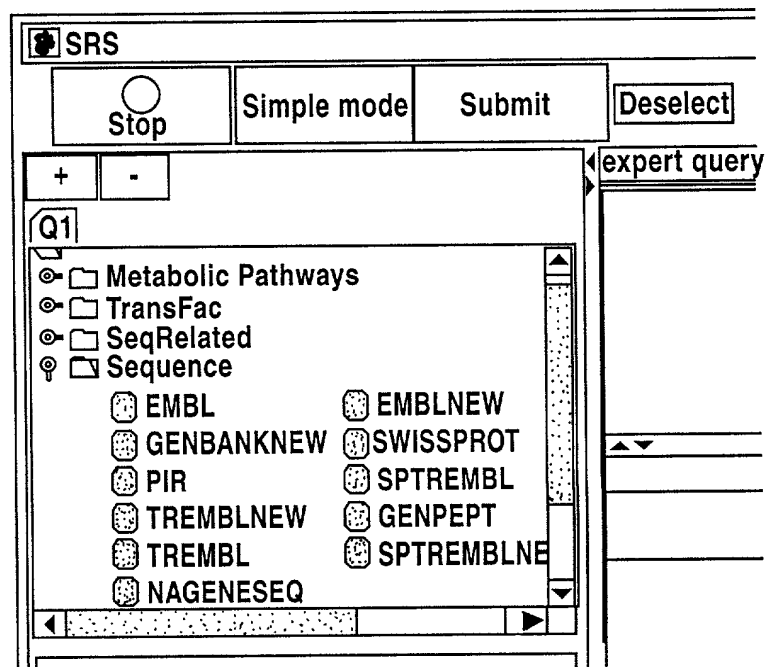


Fig.14

Gene	Description	Selected in
W72759	zd71h04.s1 Soares fetal heart NbHH19W Homo sapie...	◆
R40626	yf72g12.s1 Homo sapiens cDNA clone 28051 3'.	◆
AA001916	zh83b05.s1 Soares fetal liver spleen 1NFLS S1 Homo...	◆
R43728	yg20c12.s1 Homo sapiens cDNA clone 32811 3'.	◆
AA041370	zf09a02.s1 Soares fetal heart NbHH19W Homo sapie...	◆
T95837	ye42c02.s1 Homo sapiens cDNA clone 120386 3'.	◆
H27557	yl61g03.s1 Homo sapiens cDNA clone 162772 3' simi...	◆
AA024572	ze76h08.s1 Soares fetal heart NbHH1 9W Homo sapie...	◆

Fig.16

○

Stop

Simple mode

Submit

+

-

Q1

ys

EW

W

Q

☐ EMBLNEW
☐ SWISSPROT
☐ SPTREMBL
☐ GENPEPT
☐ SPTREMBLNEW

☐ GENBANK
☐ SWISSNEW
☐ REMTREMBL
☐ GENPEPTNEW
☐ AAGENESEQ

Description ▼

cyclin

+

-

Fig.17

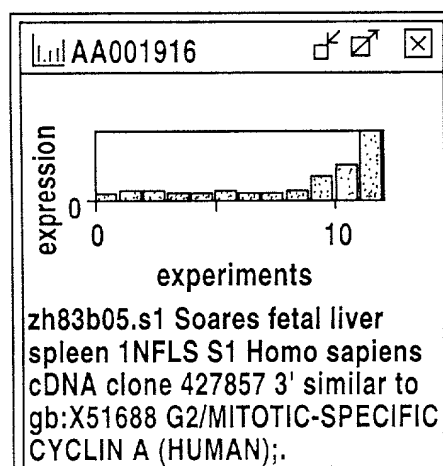
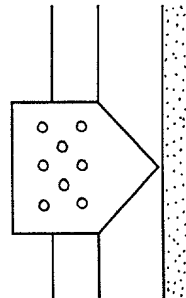
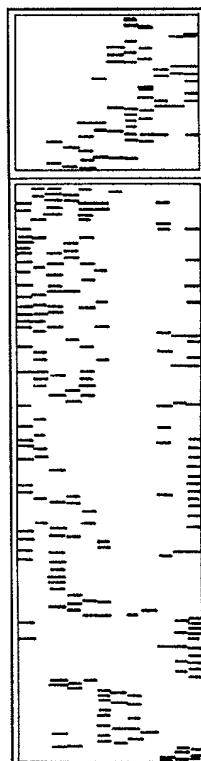


Fig.18



Scale Tab

Fig.19



Cluster 1

Cluster G

Cluster E

Cluster C

Cluster B

Cluster A

Fig.20

Projects

- ☐  **Bertrand**
- ☐  **fibroblast data**
- ☐  **Fibroblast Project**
- ☐  **Illico Presto**

Fig.21










- ☒  **Experiment group 1**
 -  **experiment 0 min**
 -  **experiment 15 min**
 -  **experiment 30 min**
 -  **experiment 1h**
 -  **experiment 2h**

Fig.22

 **Input** 

 Please input an experiment group name

Experiment group name dialog box.

Fig.23

Choose experiment class dialog box.

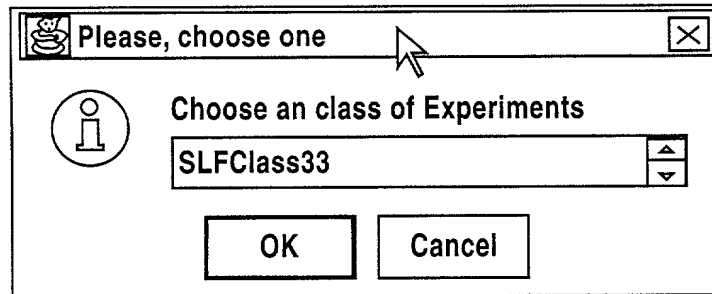


Fig.25

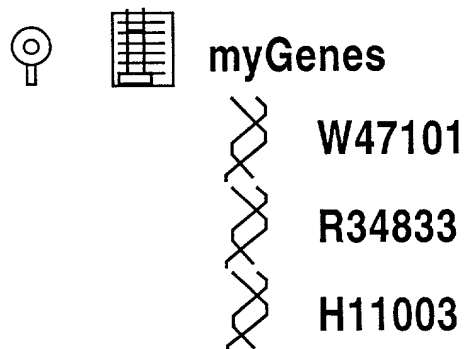


Fig.24

Add/Remove dialog box for adding and removing experiments from experiment groups.

Select experiments to add or remove

experiment 0 min
experiment 15 min
experiment 1h
experiment 4h
experiment 8h
experiment 16h
experiment 24h

<<Add<<

>>Remove>>

OK Cancel

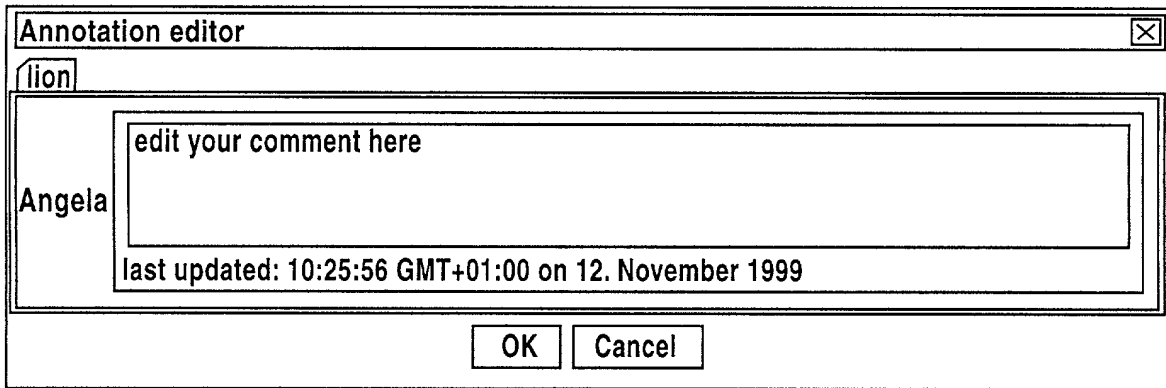
AKgroup1

Experiment Class 7

experiment 30 min
experiment 2h
experiment 6h
experiment 12h
experiment 20h
experiment unsync

Fig.26

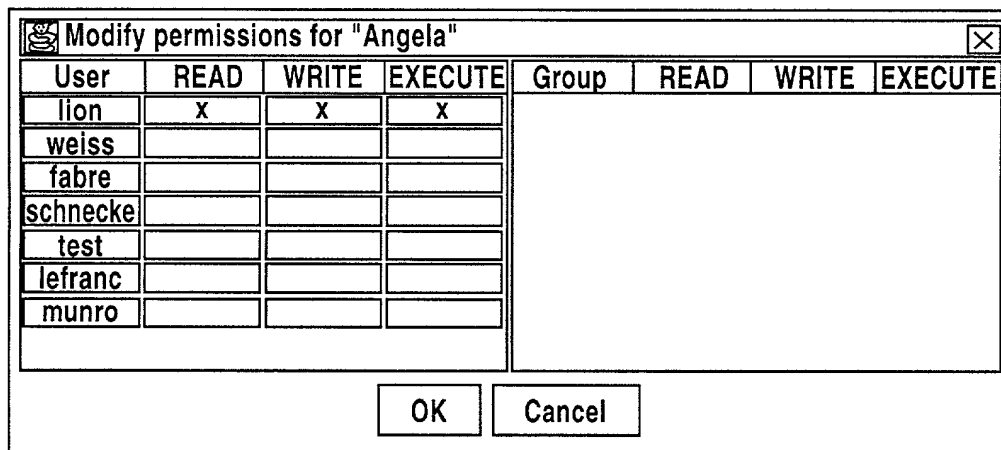
The annotation editor.



The dialog box is titled "Annotation editor". It features a tab labeled "lion". On the left, the name "Angela" is displayed. To the right of "Angela" is a large text area containing the placeholder text "edit your comment here". Below this text area, it says "last updated: 10:25:56 GMT+01:00 on 12. November 1999". At the bottom of the dialog are two buttons: "OK" and "Cancel".

Fig.27

The permissions dialog box for project "Angela".

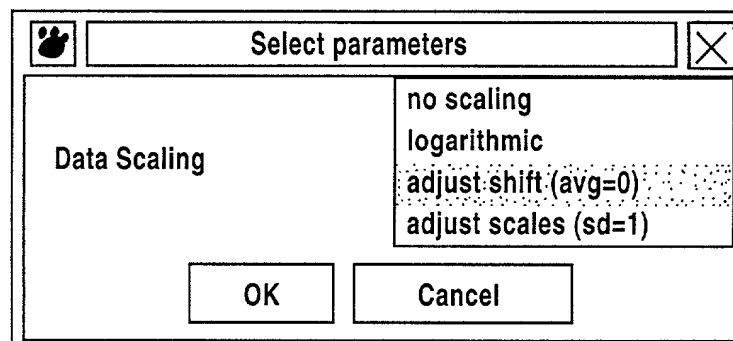


The dialog box is titled "Modify permissions for 'Angela'". It contains a table with columns for "User", "READ", "WRITE", "EXECUTE", and "Group". The "User" column lists: lion, weiss, fabre, schnecke, test, lefranc, and munro. The "READ", "WRITE", and "EXECUTE" columns have checkboxes. The "lion" row has all three checked (marked with 'x'). The "Group" column is empty. At the bottom are "OK" and "Cancel" buttons.

User	READ	WRITE	EXECUTE	Group
lion	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	
weiss	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
fabre	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
schnecke	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
test	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
lefranc	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
munro	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	

Fig.28

Select parameters "Data Scaling" dialog box.



The dialog box is titled "Select parameters". It has a "Data Scaling" label on the left. On the right, there is a list of options: "no scaling", "logarithmic", "adjust shift (avg=0)", and "adjust scales (sd=1)". The "adjust shift (avg=0)" option is highlighted with a dotted background. At the bottom are "OK" and "Cancel" buttons.

Fig.29

The Choose experiments dialog box.

Please, choose the experiments to compare

x axis

experiment 0 min

y axis

experiment 15 min

OK

Cancel

Fig.30

An example difference plot.

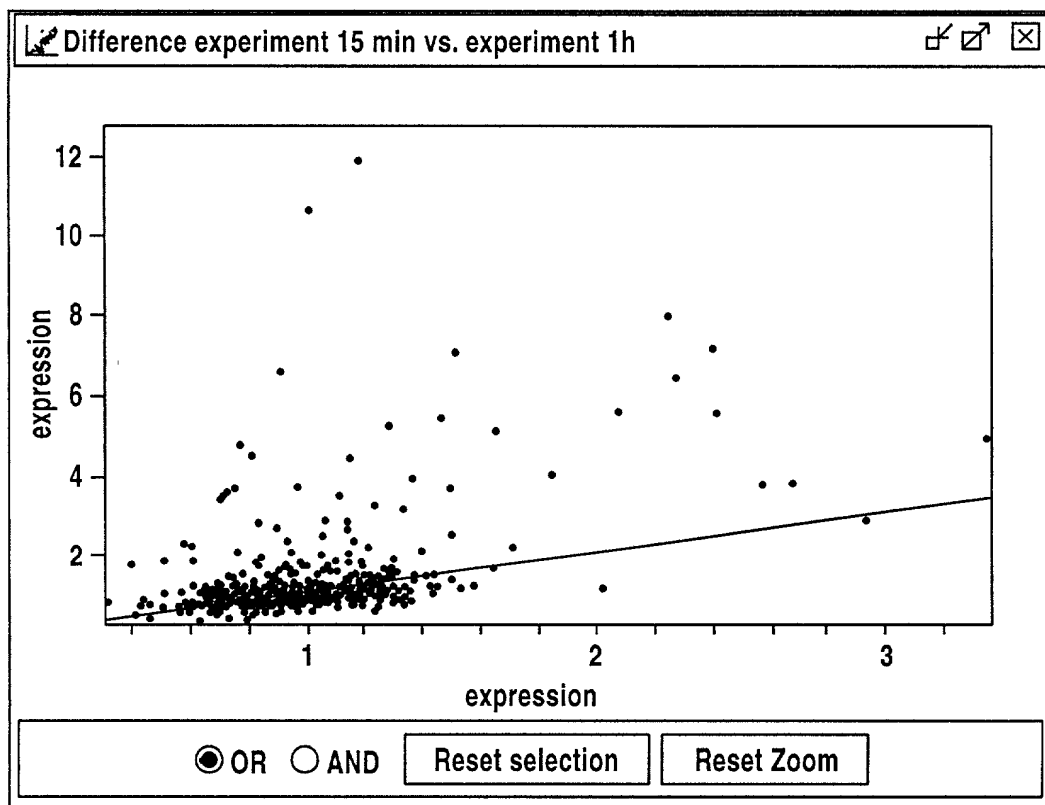


Fig.31

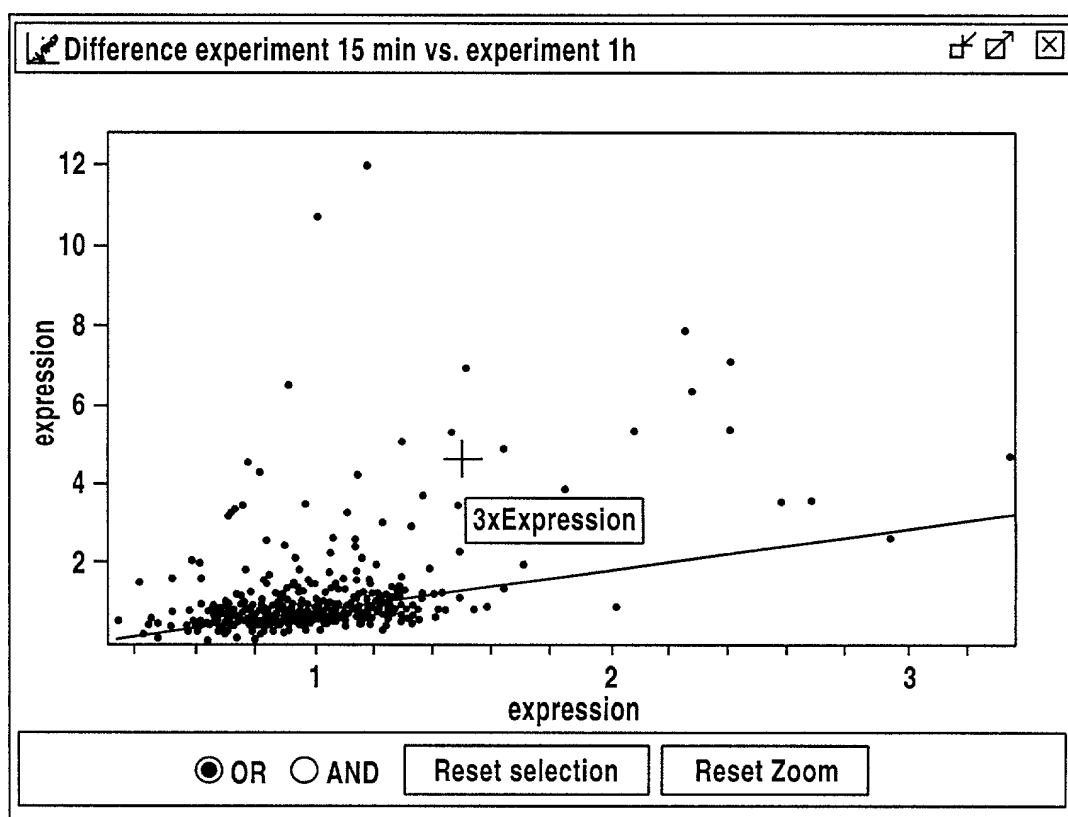


Fig.32

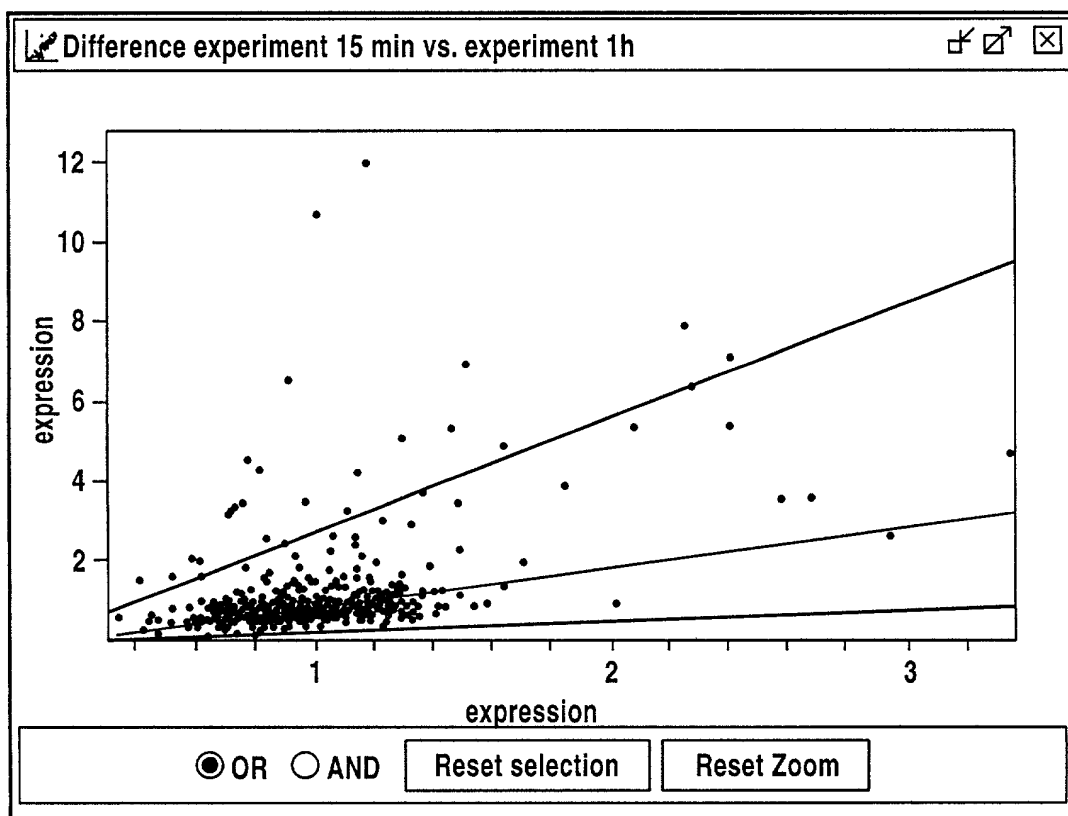


Fig.33

Select Profile Patterns dialog box.

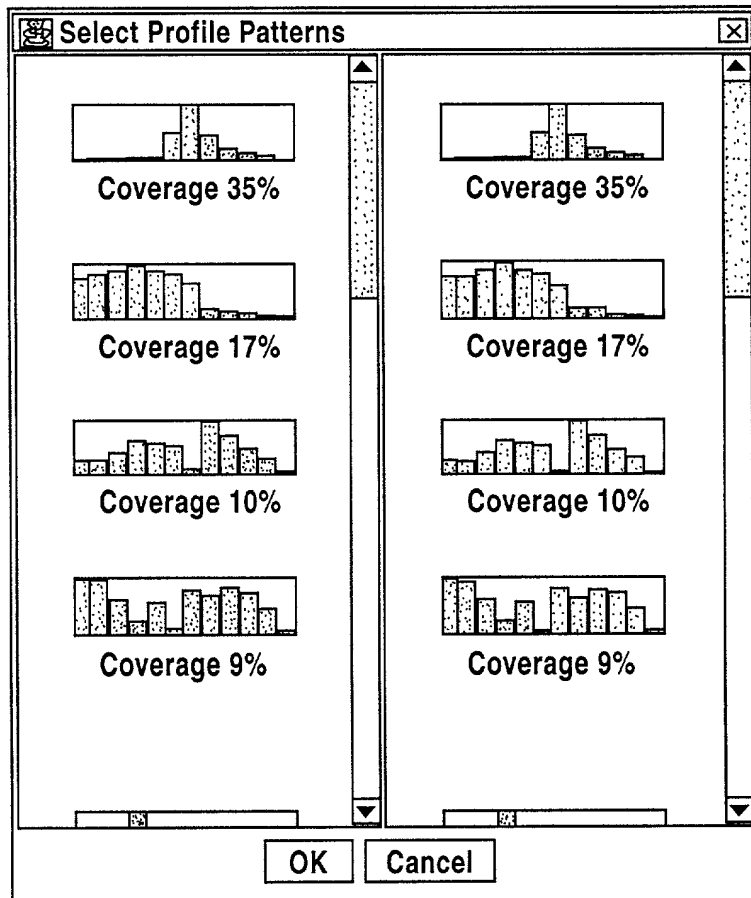


Fig.34

Gene profiled in Fig.35
Distance Plot created with the adjust shift (avg=0) scaling procedure
and the patterns displayed in Fig.33

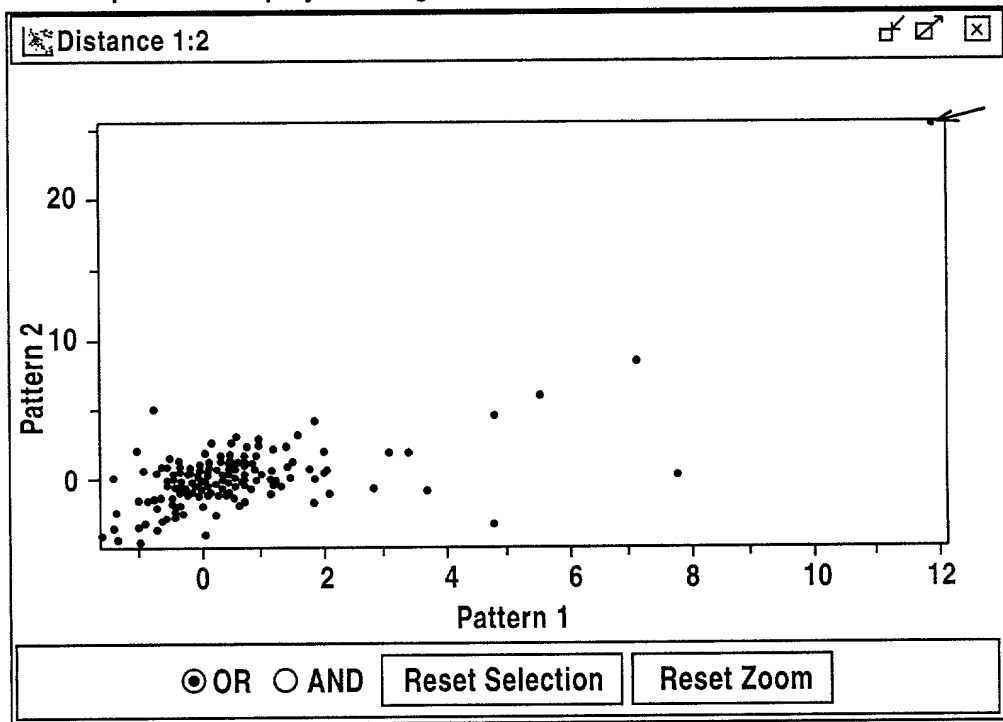
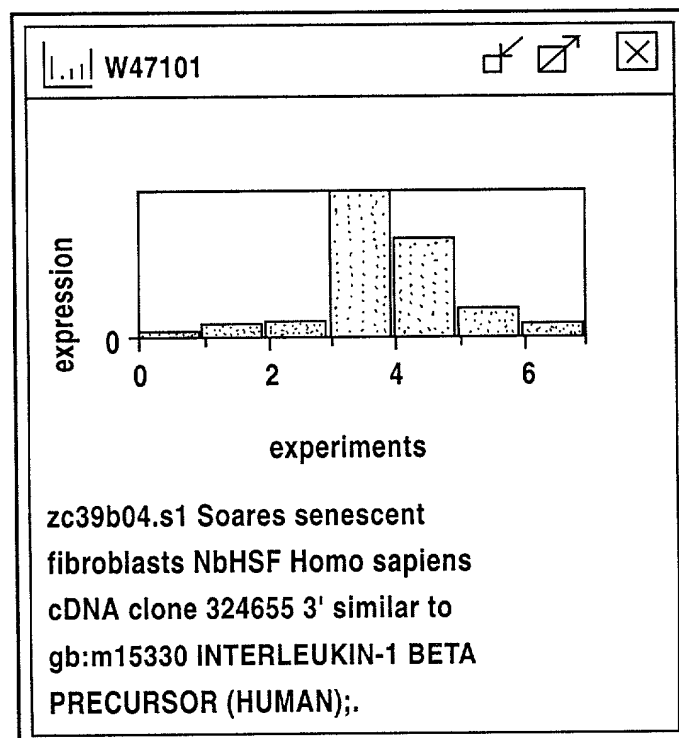


Fig.35



Gene Profile of gene W47101 plotted at (12,26) in the above Distance Plot (Figure 34).

Fig.36

The "Select Experiments to plot" dialog box for the variance histogram.

Experiment	Include	Exclude
experiment I	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment II	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment III	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment IV	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment V	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment VI	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment VII	<input checked="" type="checkbox"/>	<input type="checkbox"/>

OK Cancel

Fig.37

The Variance Histogram with two bars selected.

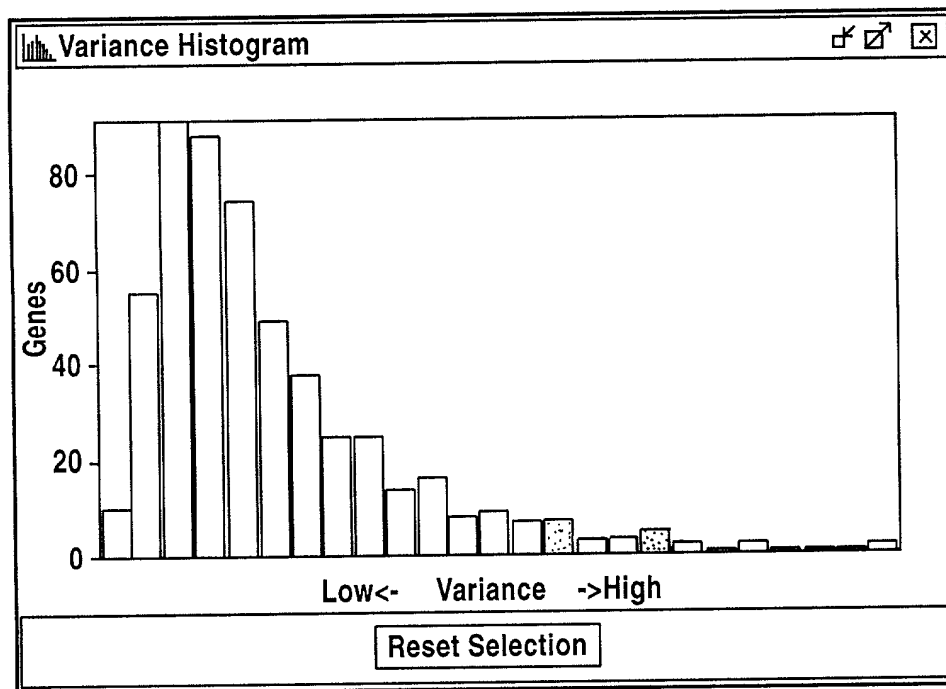


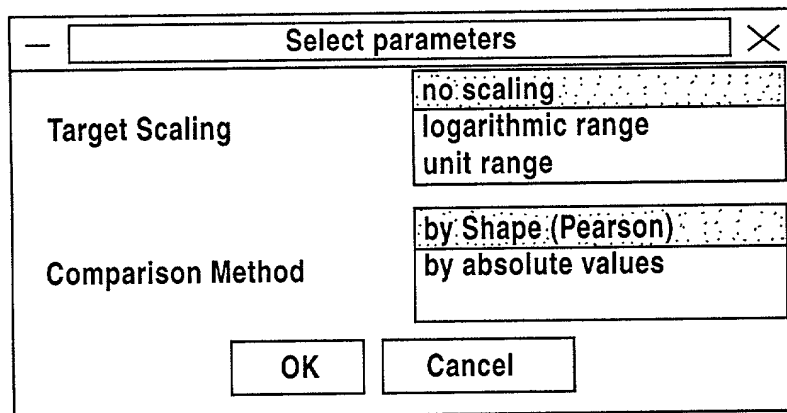
Fig.38

The "Enter Correlation Values" dialog box.

Enter Correlation value	
Experiment	Target Value
experiment 0 min	1
experiment 15 min	1
experiment 30 min	1
experiment 1h	1
experiment 2h	1
experiment 4h	1
experiment 6h	1
experiment 8h	1
experiment 12h	10.0
experiment 16h	1
experiment 20h	1
experiment 24h	1

Fig.39

Correlation histogram parameters dialog box.



A dialog box titled "Select parameters" with a close button (X) in the top right corner. It contains two main sections: "Target Scaling" and "Comparison Method". The "Target Scaling" section has three options: "no scaling" (selected with a dotted background), "logarithmic range", and "unit range". The "Comparison Method" section has two options: "by Shape (Pearson)" (selected with a dotted background) and "by absolute values". At the bottom, there are "OK" and "Cancel" buttons.

Parameter	Selected Option
Target Scaling	no scaling
Comparison Method	by Shape (Pearson)

Fig.40

A correlation histogram created using the "no scaling" and the "by Shape (Pearson)" parameters.

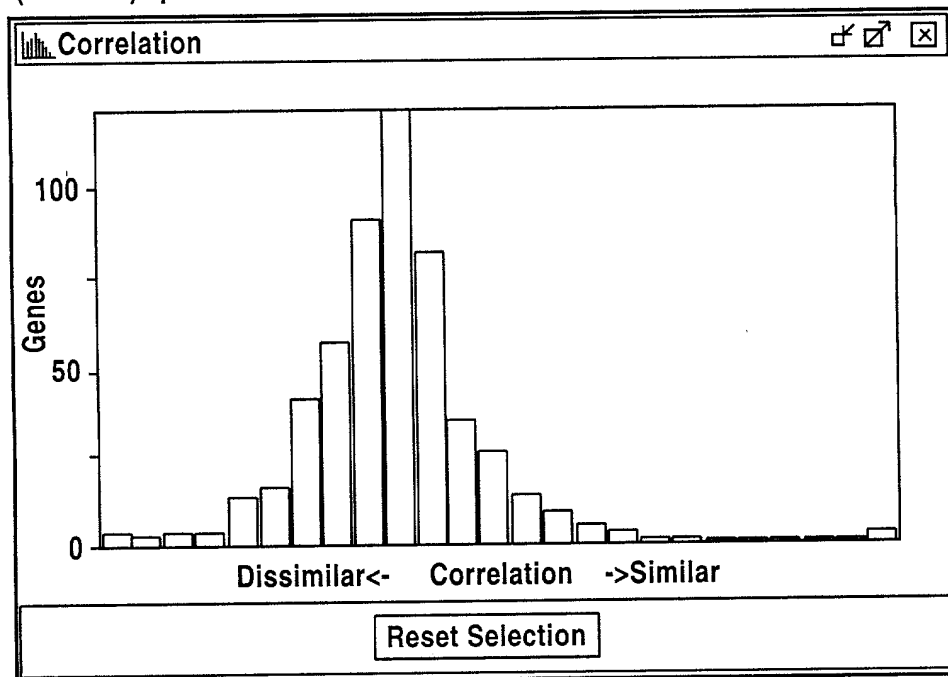


Fig.41

The "Classify Experiments" dialog box.

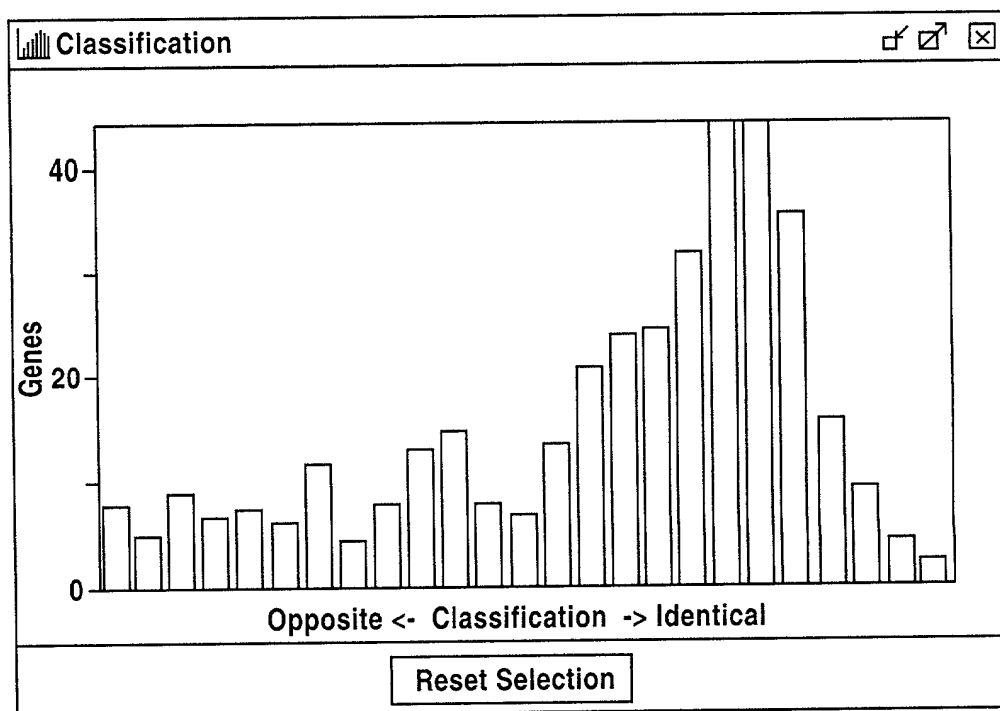
Classify Experiments

Experiment	Positive	Negative	Exclude
WT, liquid (ave)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
WT (ave)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
WT, solid (ave)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
KO (ave)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

OK

Cancel

Fig.42



The Classification histogram created using the "adjust scales" scaling procedure and the data displayed in the "Classify Experiments" dialog box above (Figure 41).

Fig.43

Select reference state dialog box.

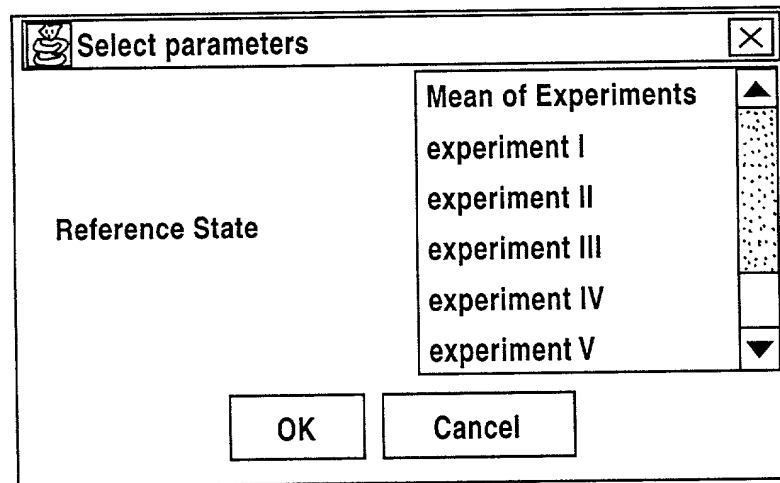


Fig.44

The Cluster Tree analysis view.

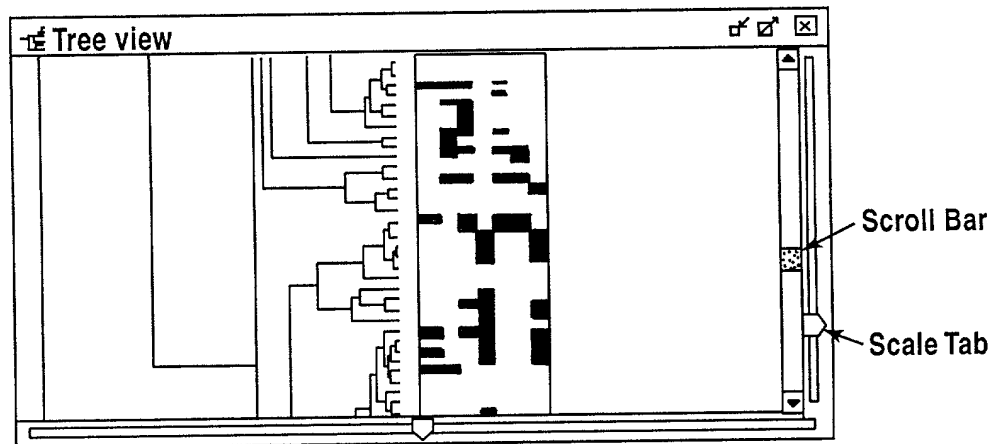



Fig.45

The SRS Interface In Simple Mode.

 SRS

☐

Stop

Detail mode

Submit

Deselect

Query on pathway

Query on swissprot alone

retrieve possible human sequences

retrieve sequences with nucleotide b

search mutation database

keyword:

Query on swissprot alone

Num	Db	ID	Description
1	SWISSPROT	AC01_YEAST	
2	SWISSPROT	ACR1_YEAST	
3	SWISSPROT	ACR3_YEAST	
4	SWISSPROT	ADB1_YEAST	
5	SWISSPROT	ADB2_YEAST	

BACK

FORWARD

Fig.46

SRS

+

-

Stop

Simple mode

Submit

Deselect

Q1

all dbs

Metabolic Pathways

TransFac

SeqRelated

Sequence

EMBL

GENBANKNEW

PIR

TREMBLNEW

TREMBL

EMBLNEW

SWISSPROT

SPTREMBL

GENPEPT

SPTREMBLNEW

Query on swissprot alone

Num	Db	ID
1	SWISSPROT	AP17_YEAST
2	SWISSPROT	FTR1_YEAST
3	SWISSPROT	IM17_YEAST
4	SWISSPROT	IM22_YEAST
5	SWISSPROT	IM23_YEAST
6	SWISSPROT	IM44_YEAST
7	SWISSPROT	IMD1_YEAST

[http://bssever1/srs6bin/cgi-bin/wgetz?-e+\[SWISSPROT-ID:IM17_YEAST\]](http://bssever1/srs6bin/cgi-bin/wgetz?-e+[SWISSPROT-ID:IM17_YEAST])

Back

Forward

SWISSPROT:IM17_YEAST

ID

IM17_YEAST

AC

P39515; Q02310;

DT

01-FEB-1995 (Rel. 31, Created)

DT

01-FEB-1995 (Rel. 31, Last sequence update)

DT

15-JUL-1998 (Rel. 36, Last annotation update)

DE

MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE S

DE

(MITOCHONDRIAL PROTEIN IMPORT PROTEIN 2) (MITOCHO

DE

PROTEIN MIM17).

GM

TIM17 OR MPI2 OR MIM17 OR SMS1 OR Y.JL143W OR JO64

STANDARD:

PRT: 158 AA.

Description

membrane

+

-

The software SRS interface in Detail Mode displaying a completed query and a database entry.

Fig.47

RDB and text Files [*.rdb and*.txt]

No file selected...

Existing class Define a new class experiment

New class name

Type of class

No identifiers File selected

Add an identifiers file

Experiment name

Select a File... Import... Cancel

Fig.48

RDB and text Files [*.rdb and*.txt]

No file selected...

Existing class Define a new class experiment

List of the existing experiment classes

- dkfz data, average
- dkfz data
- tabTestData
- Ustilago MTP
- Ustilago

Experiment name

Select a File... Import... Cancel

Fig.49

Change configuration dialog box.

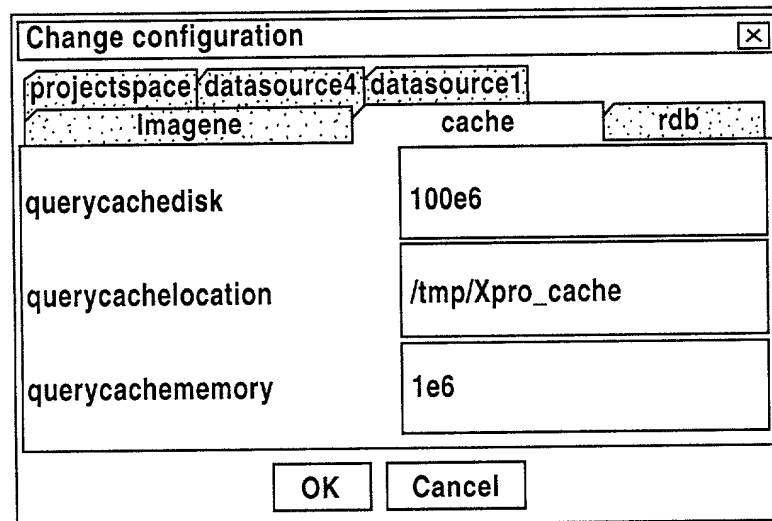


Fig.50

Remove experiment class dialog box.

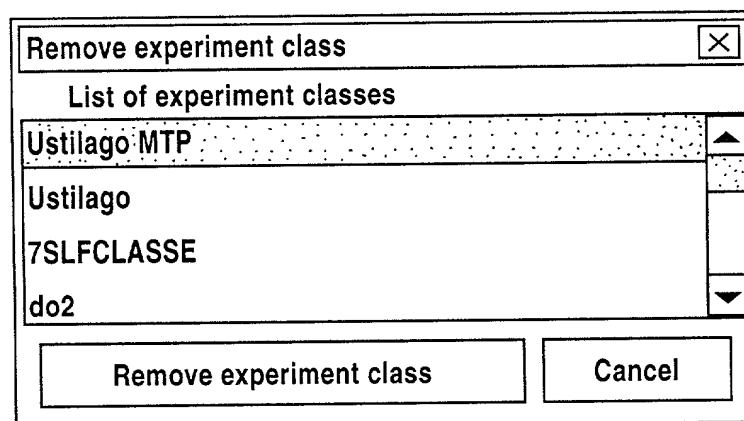


Fig.51

Remove experiments dialog box.

Remove experiments

List of experiment classes

Ustilago MTP

Ustilago

List of all experiments for the selected class

MTP-OD0_5-c

MTP-WT-a

MTP-WT-b

MTP-WT-ave

Remove experiments

Cancel

Fig.52

A point (gene) plotted in three dimensions.

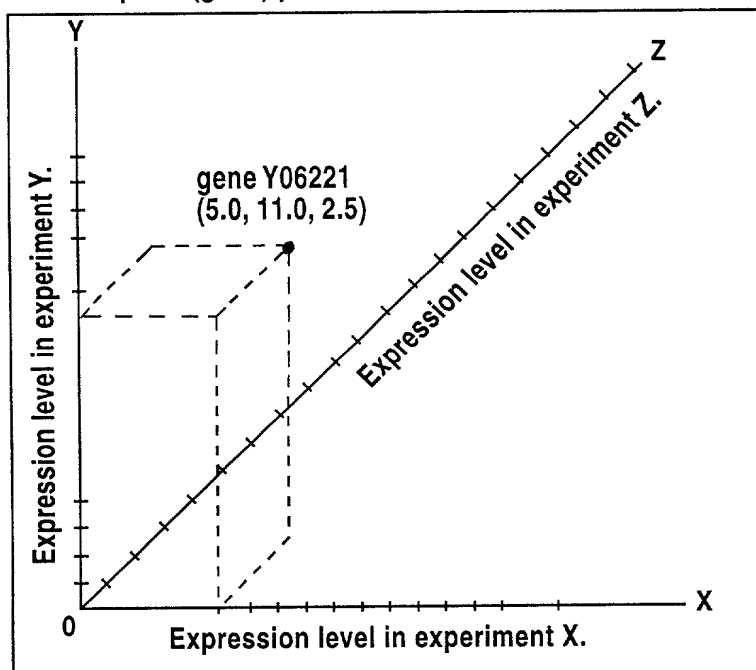


Fig.53

Three experiments plotted in 3 dimensions.

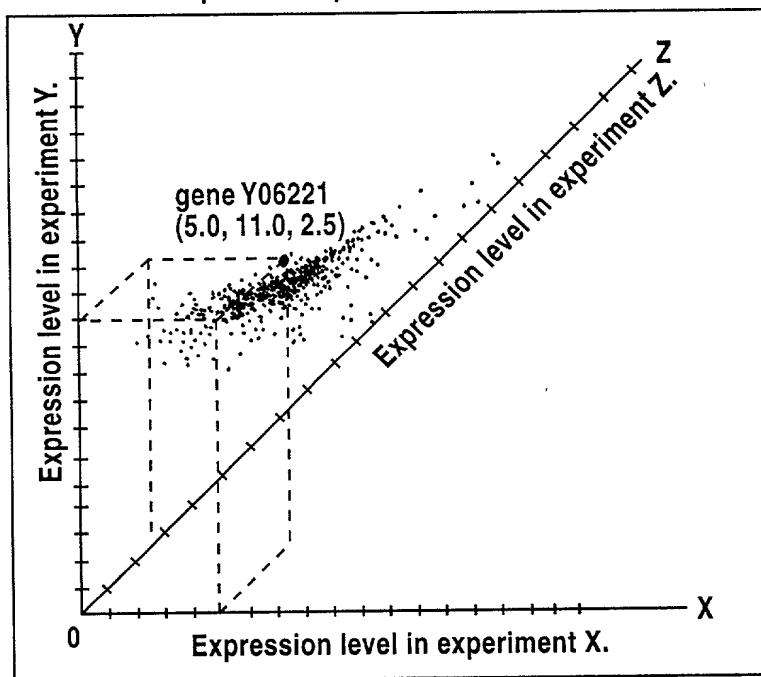


Fig.54

Squash the cigar along its side to best preserve its shape.

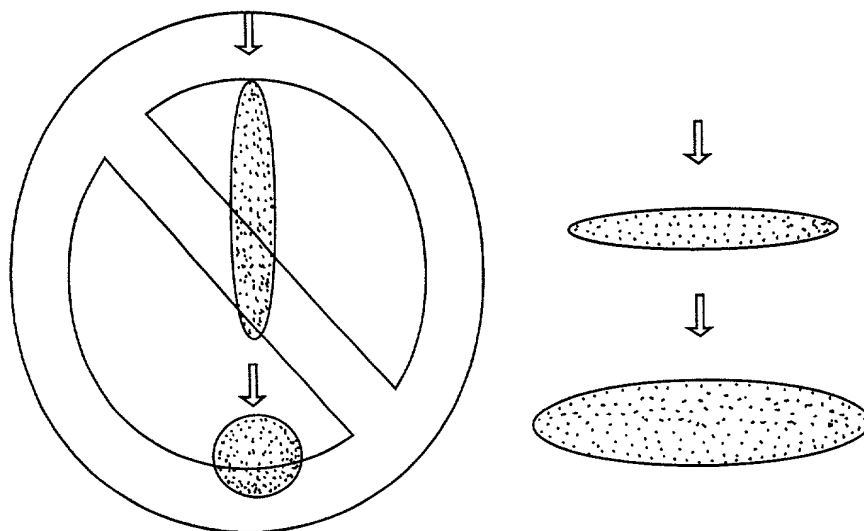


FIG.55

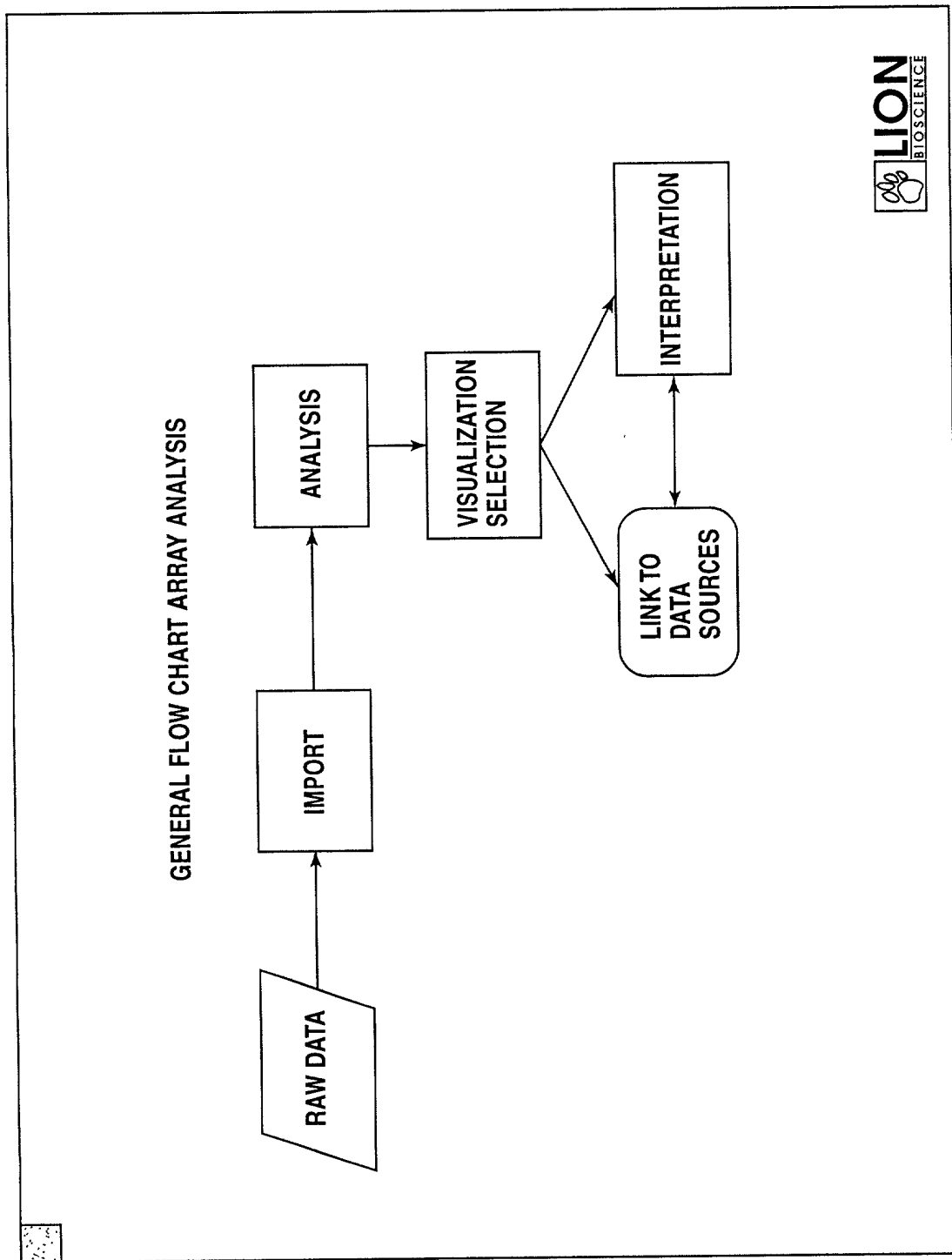


FIG.56

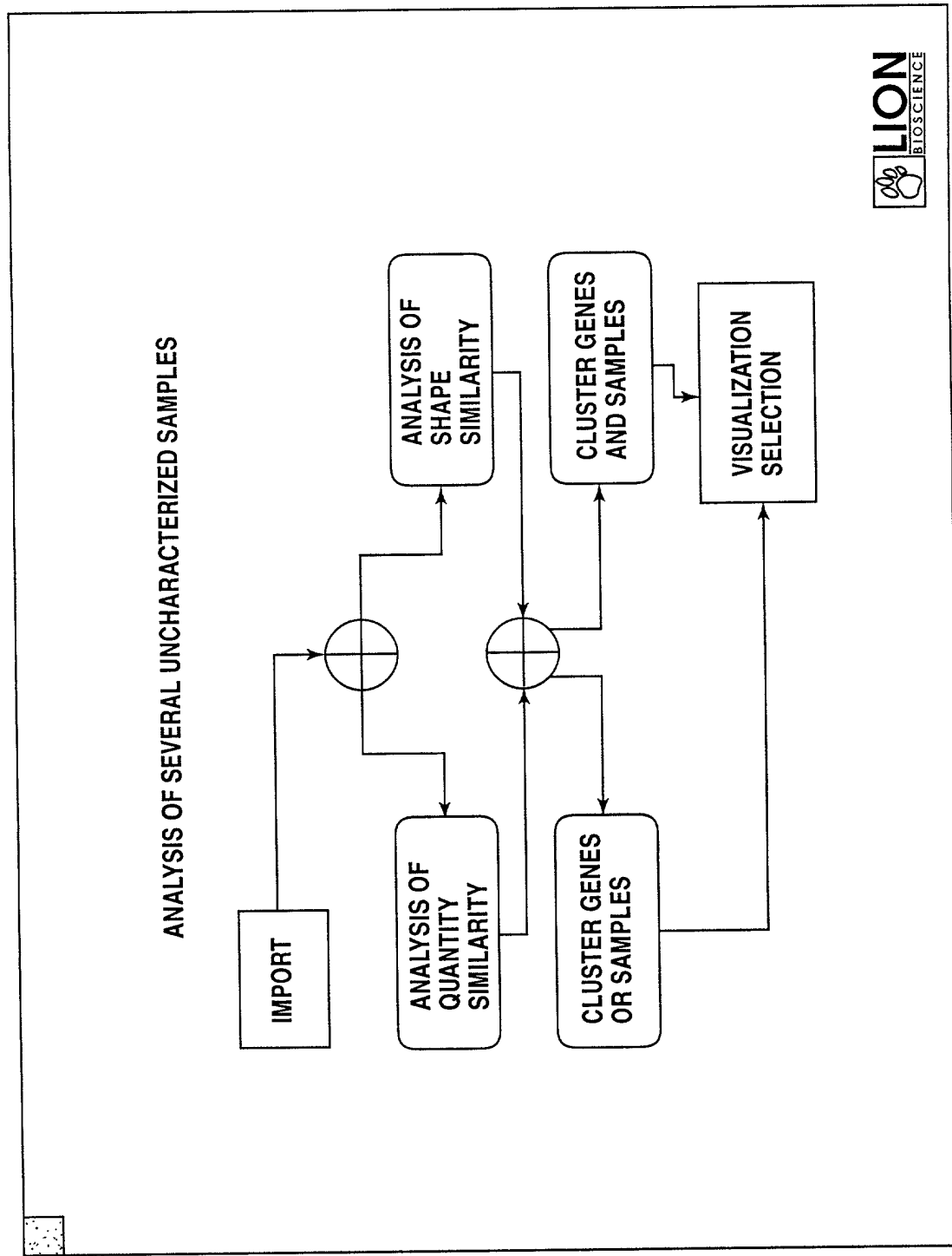


FIG.57

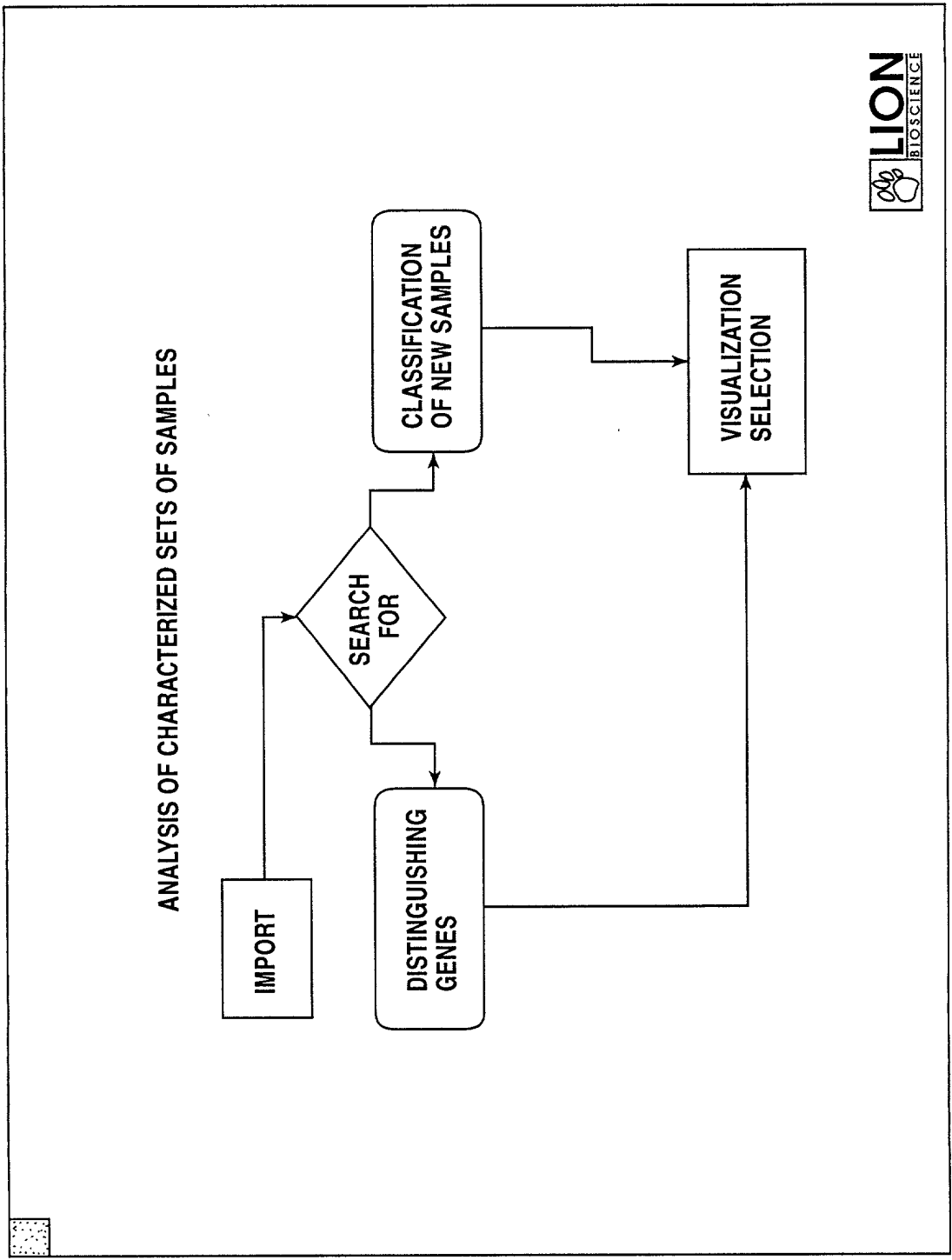


FIG.58

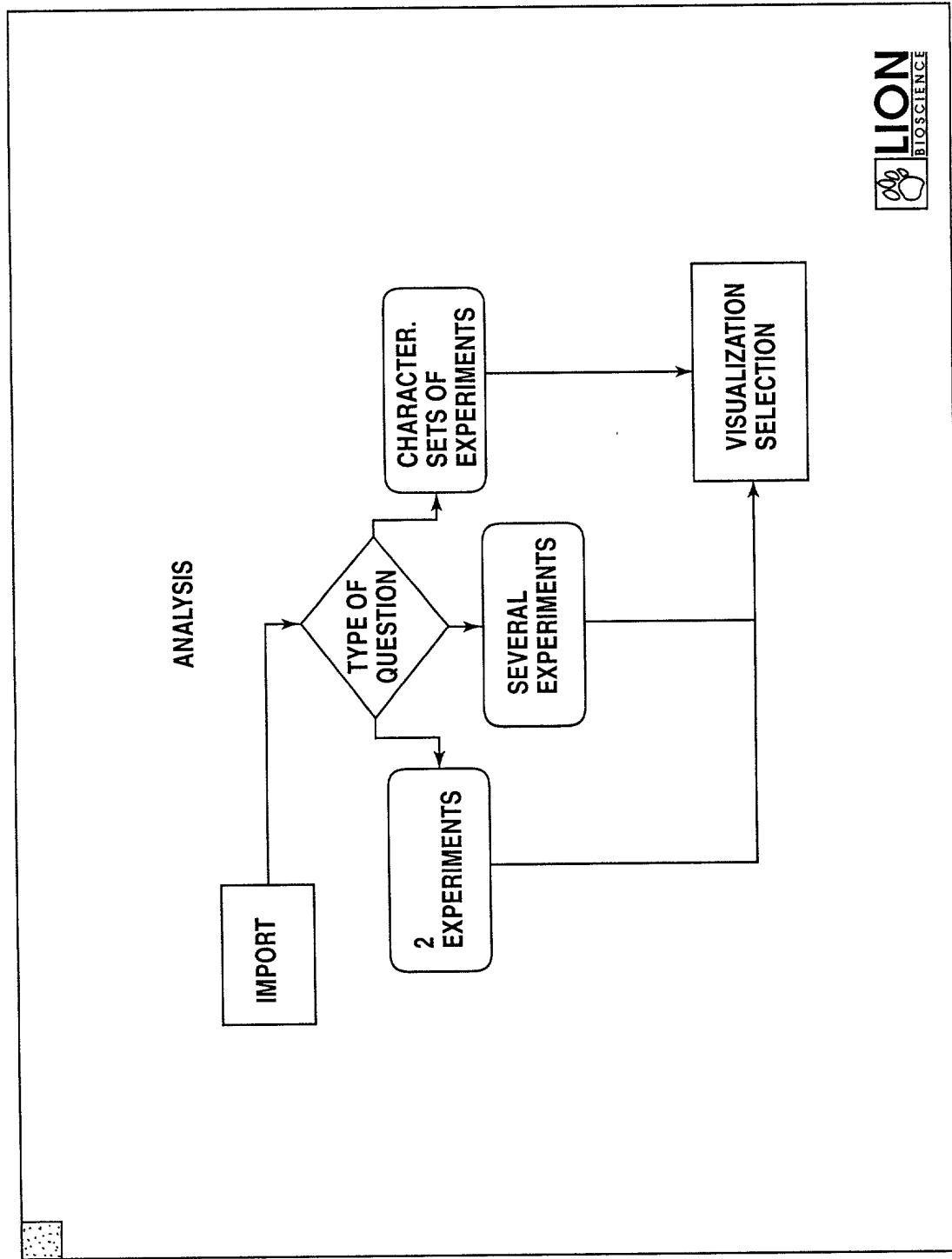


FIG.59

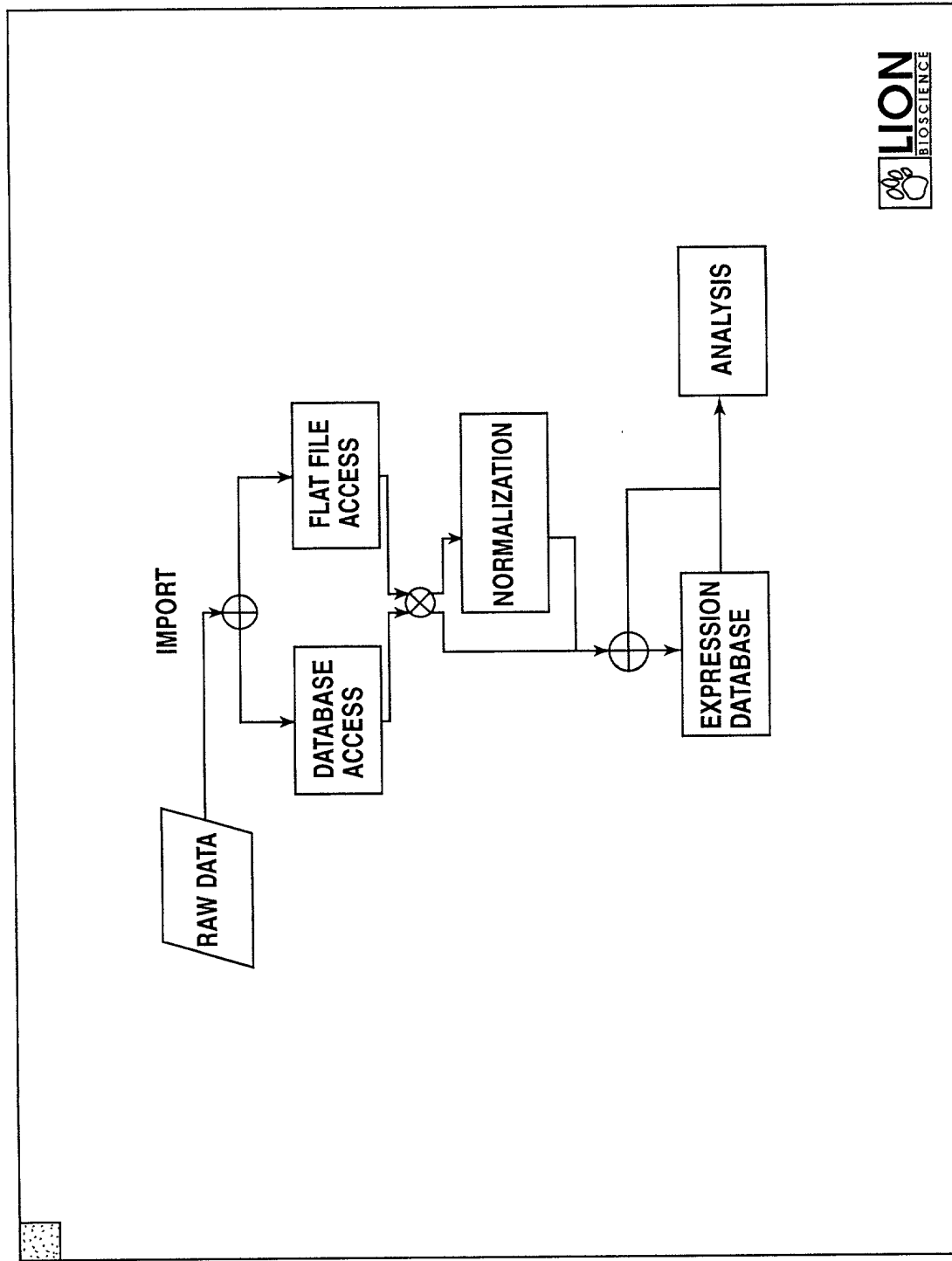
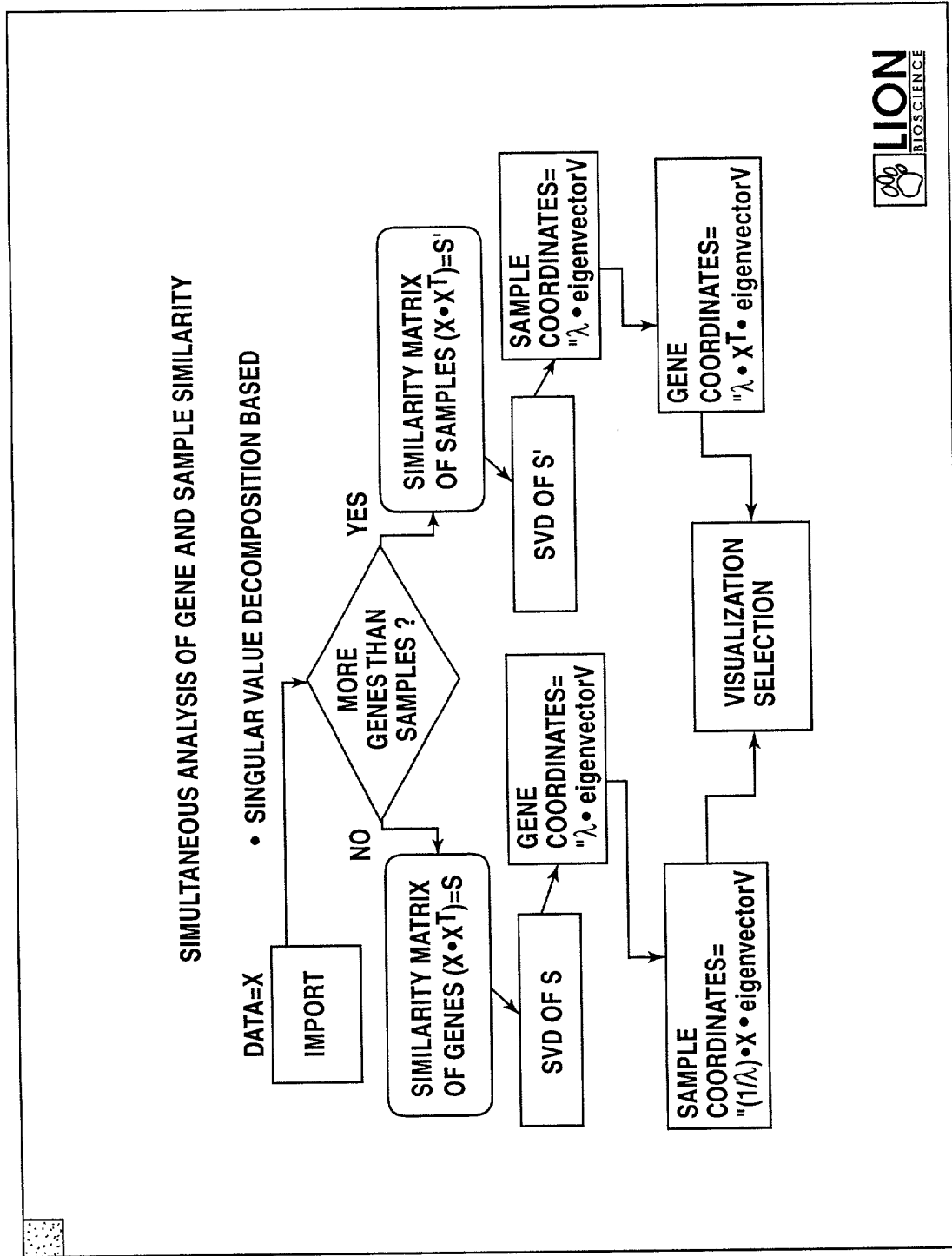


FIG.60



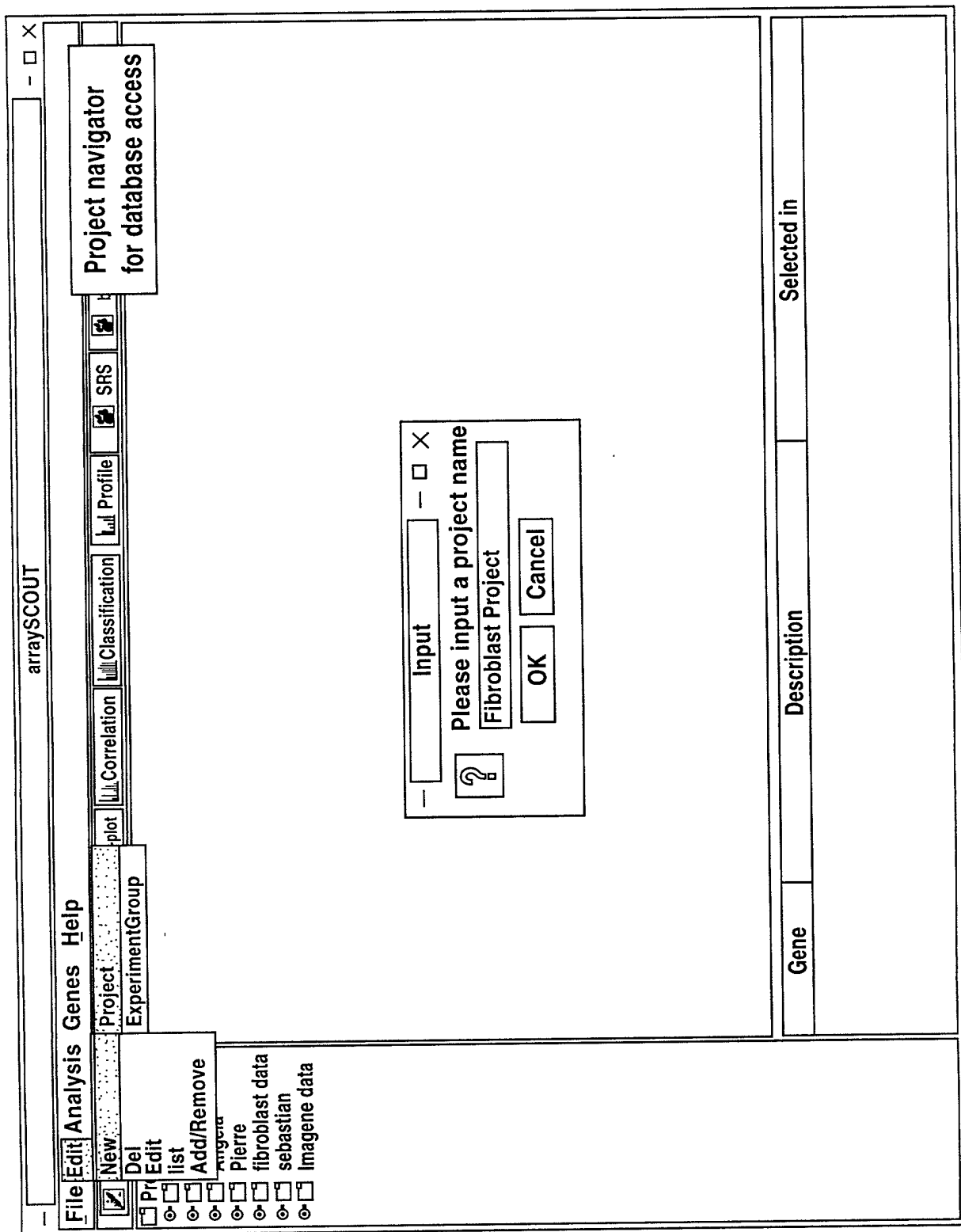


FIG.61

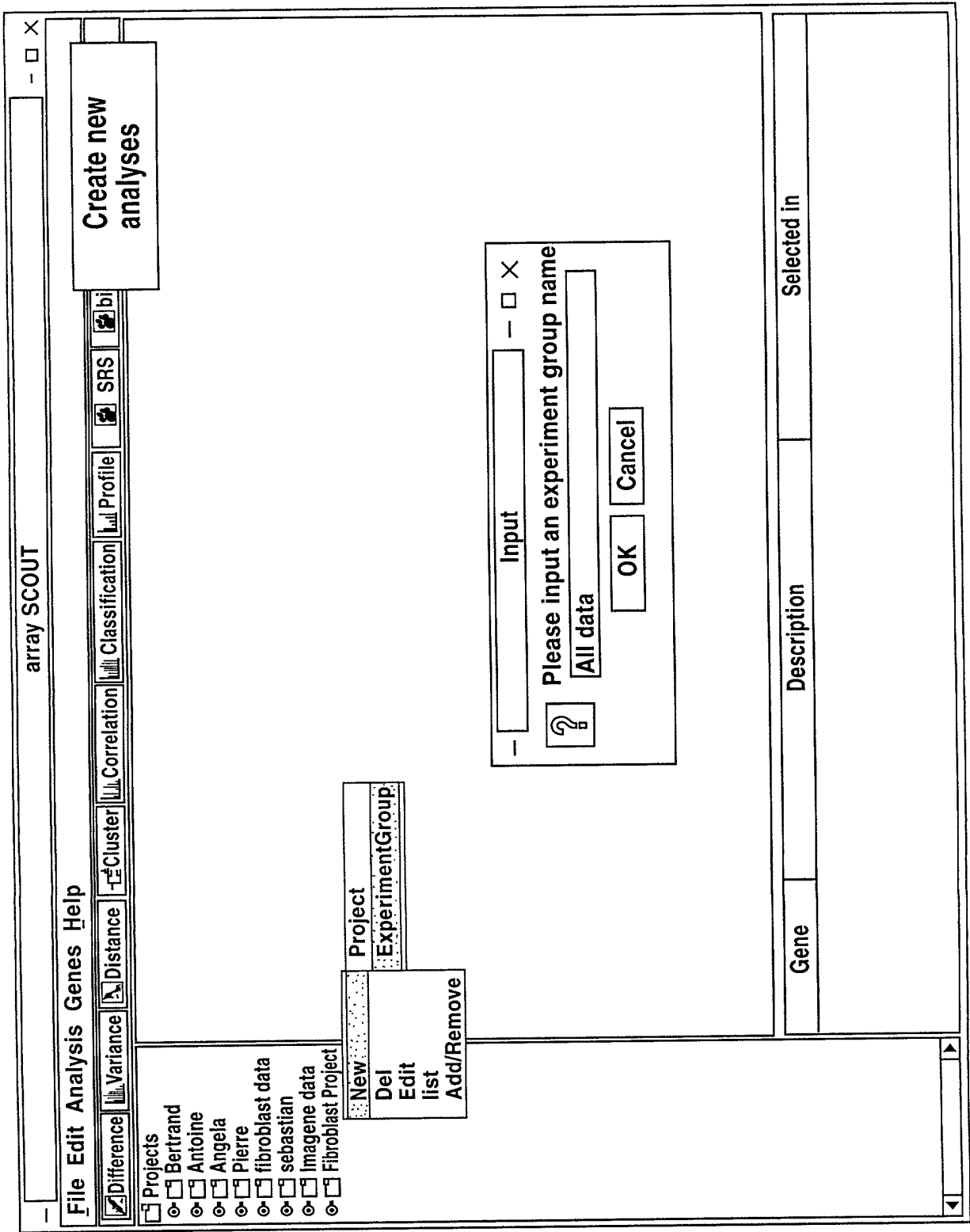


FIG.62

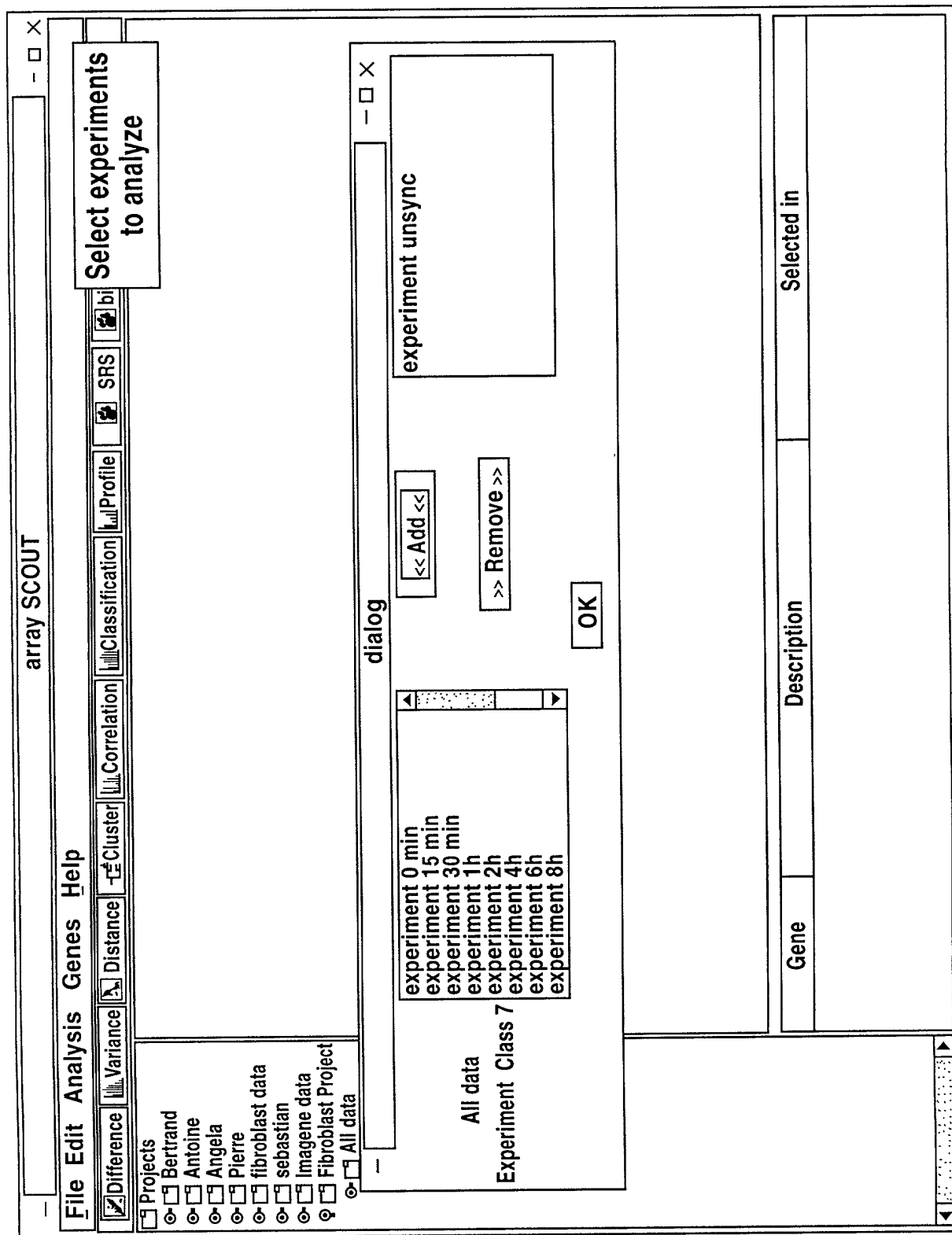


FIG.63

FIG.64

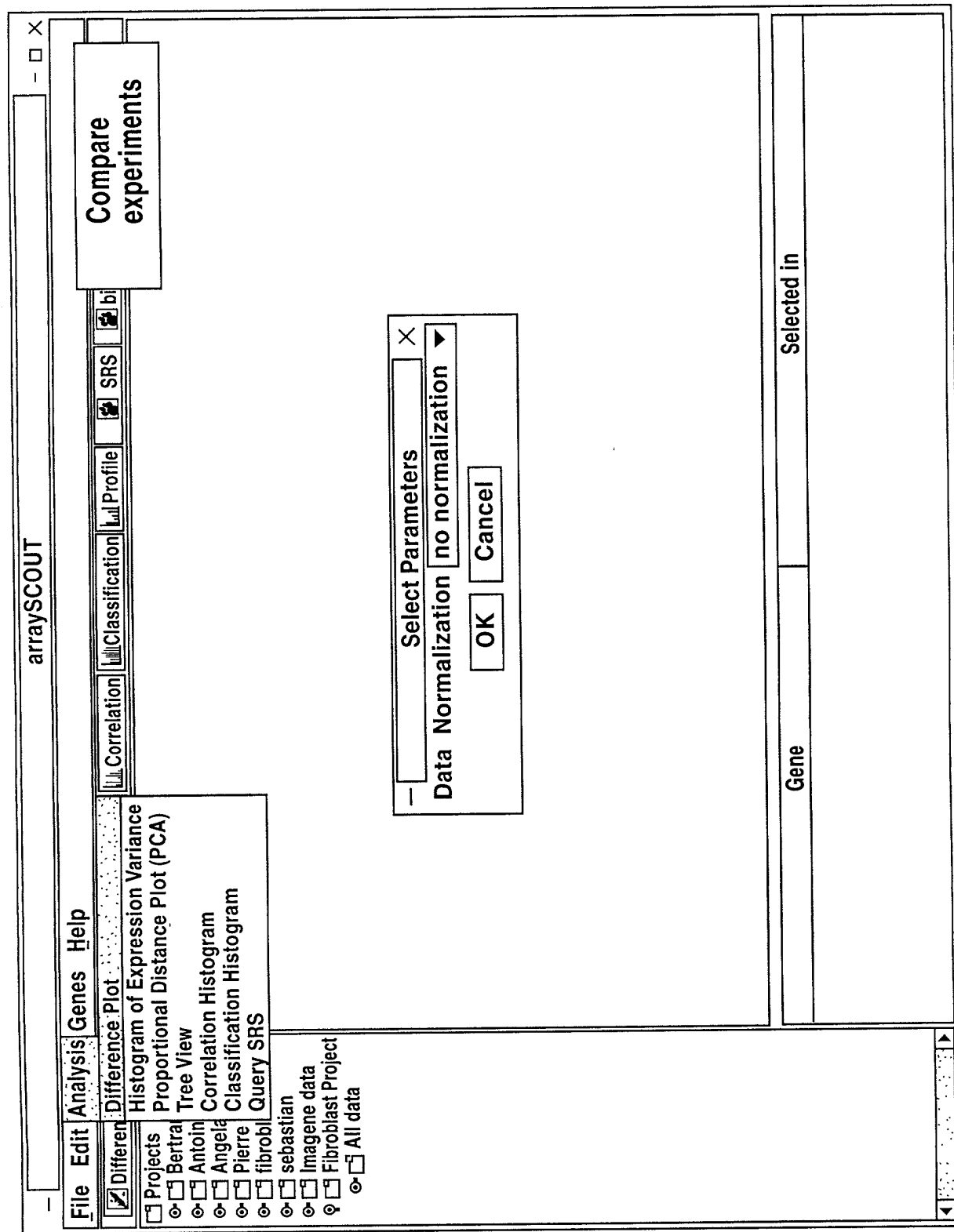


FIG.65

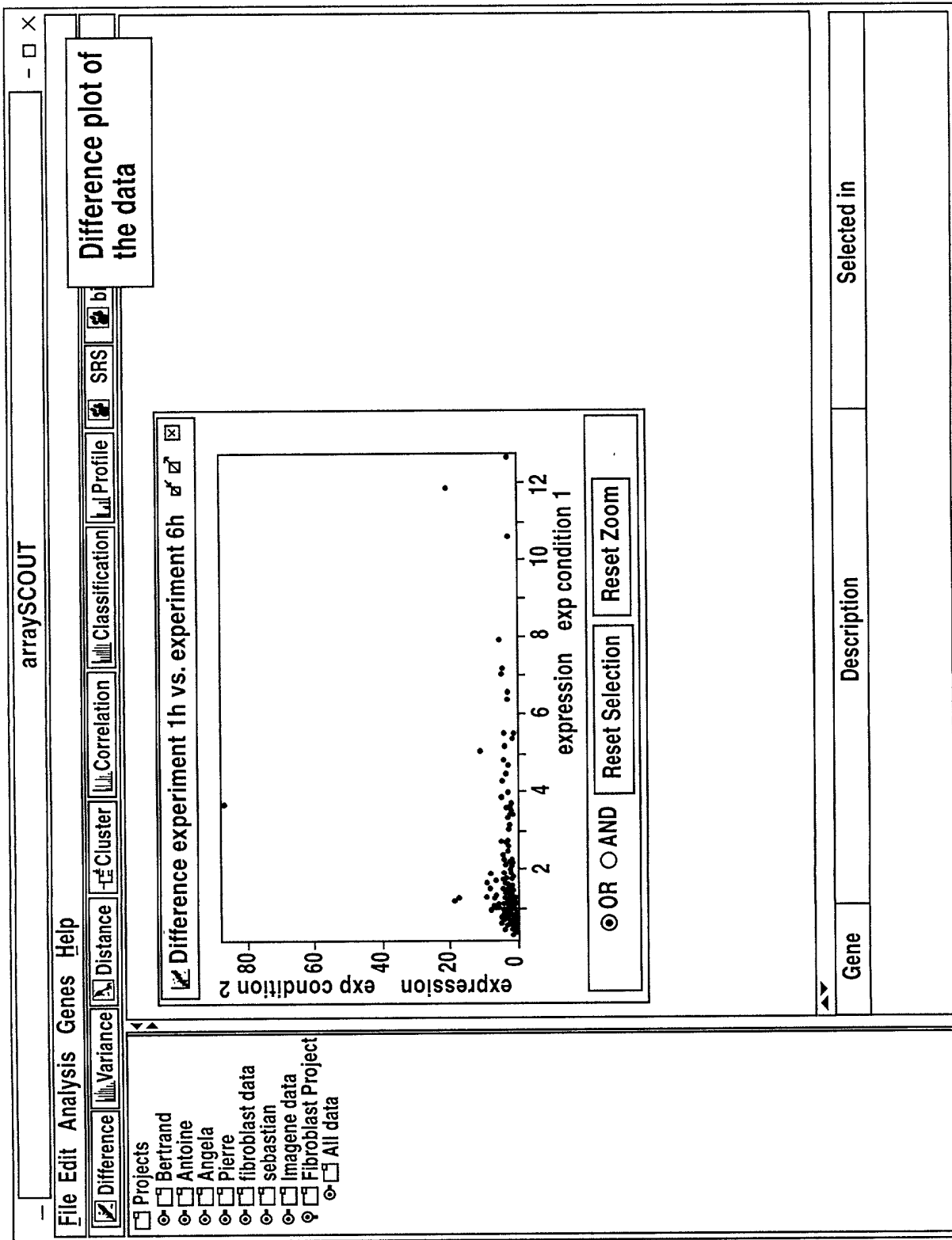
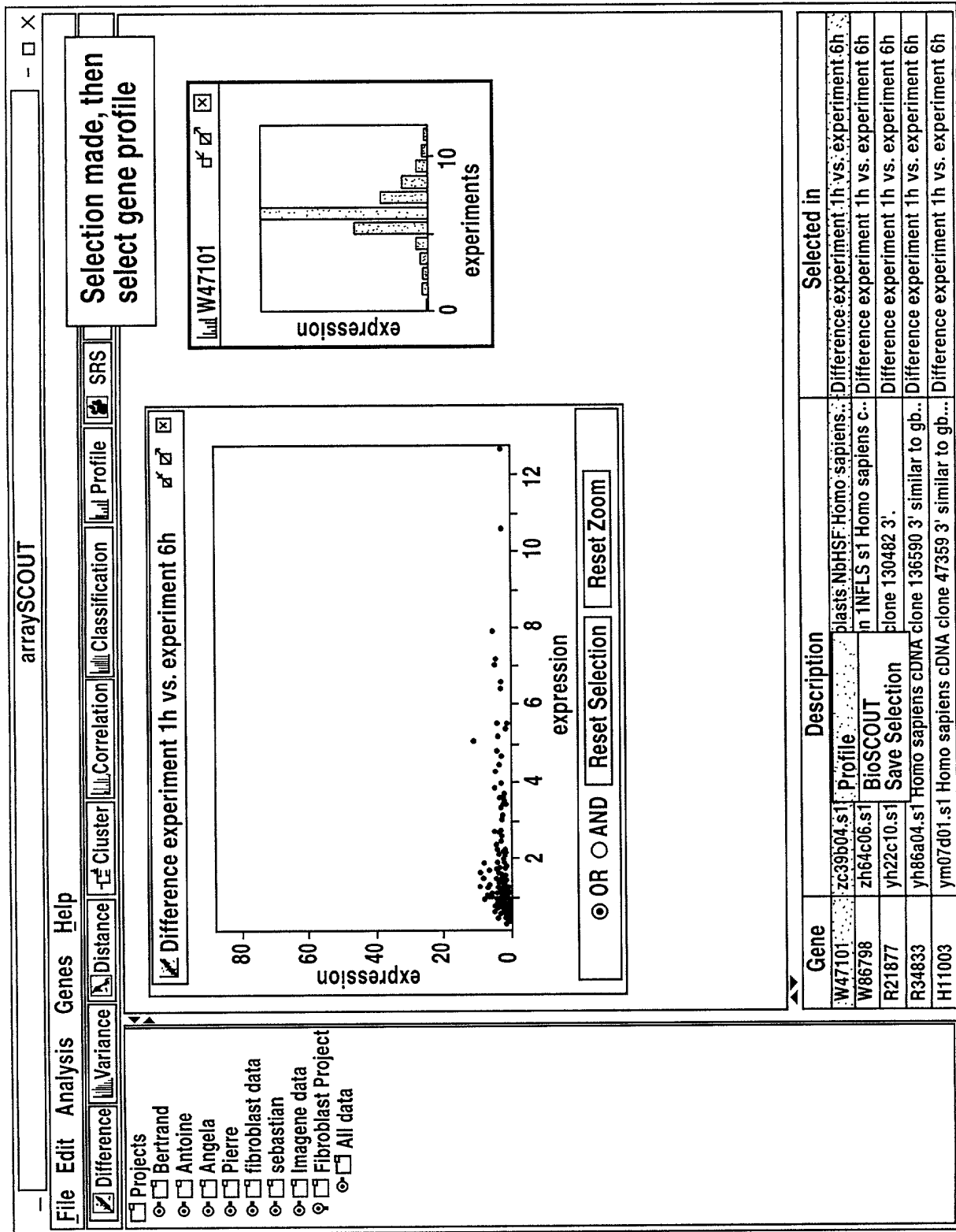
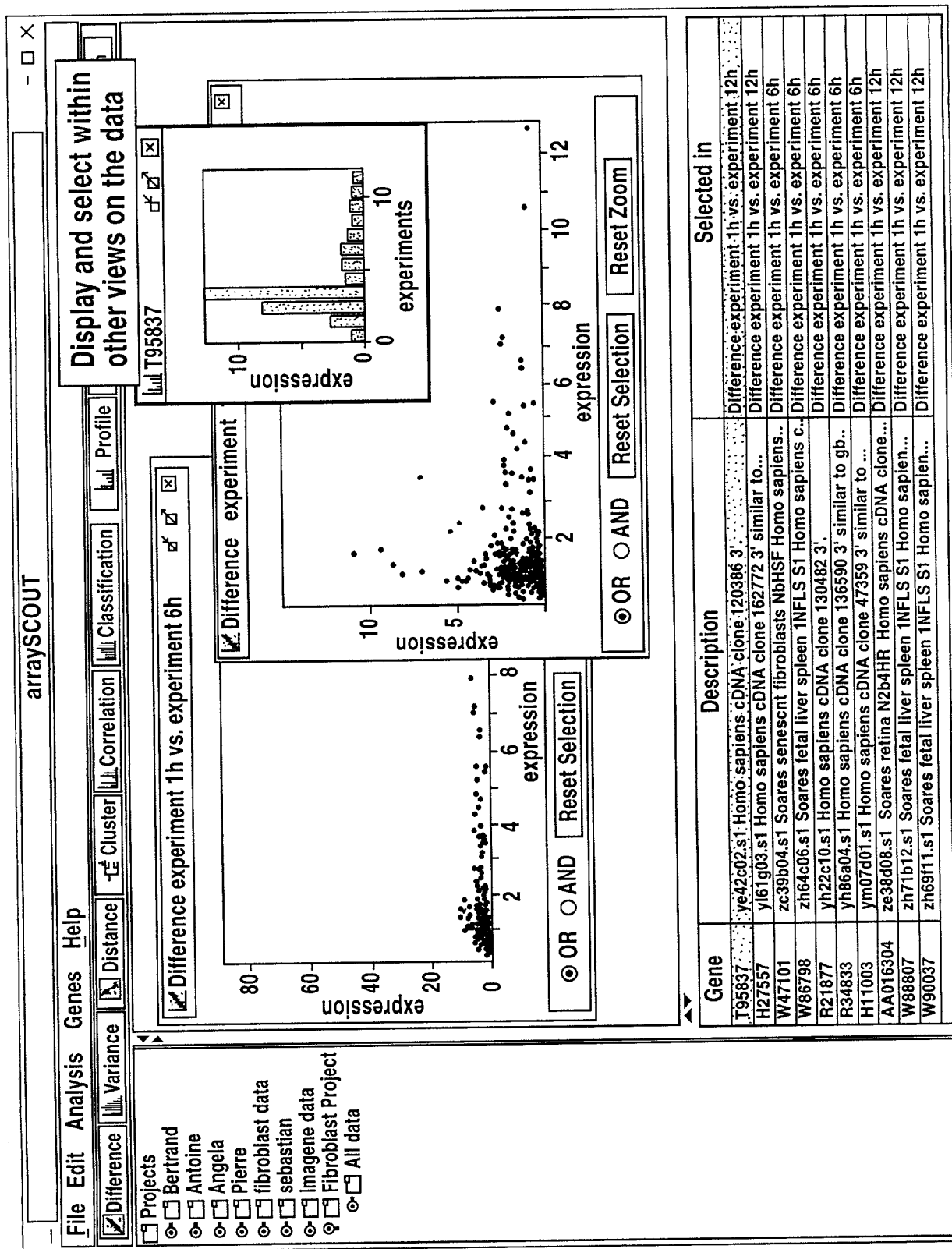


FIG.66





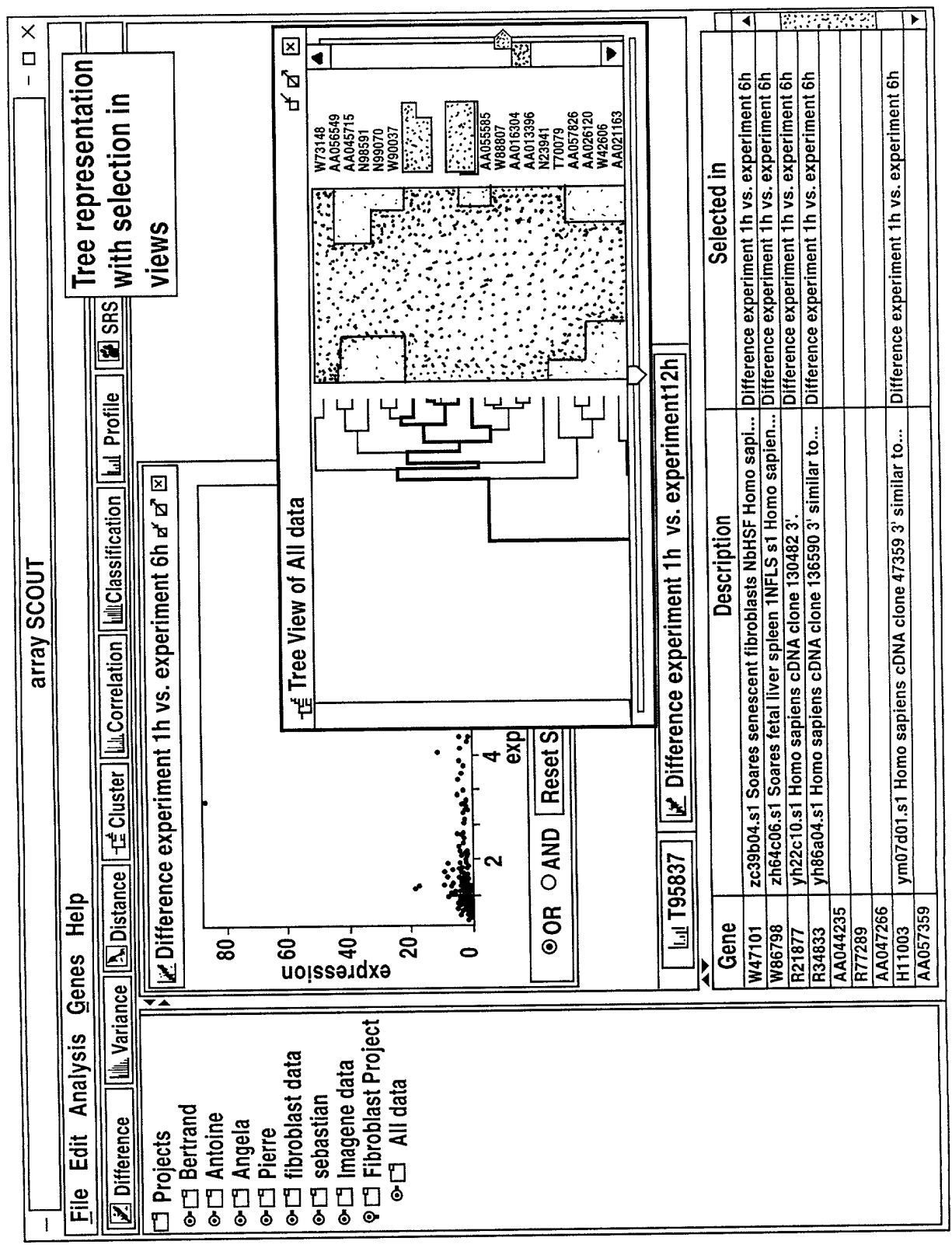


FIG.68

FIG. 69

FIG.70

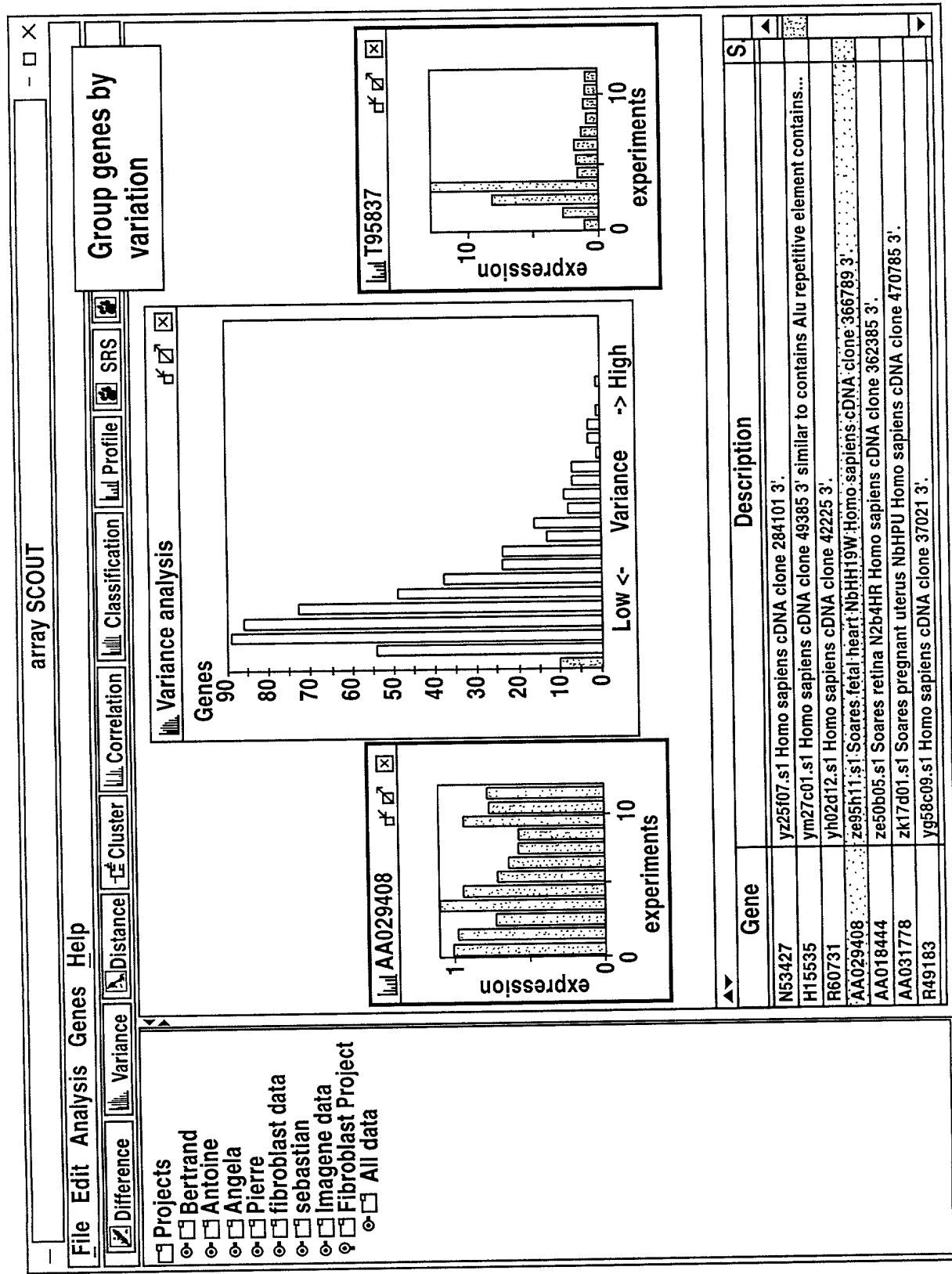


FIG.71

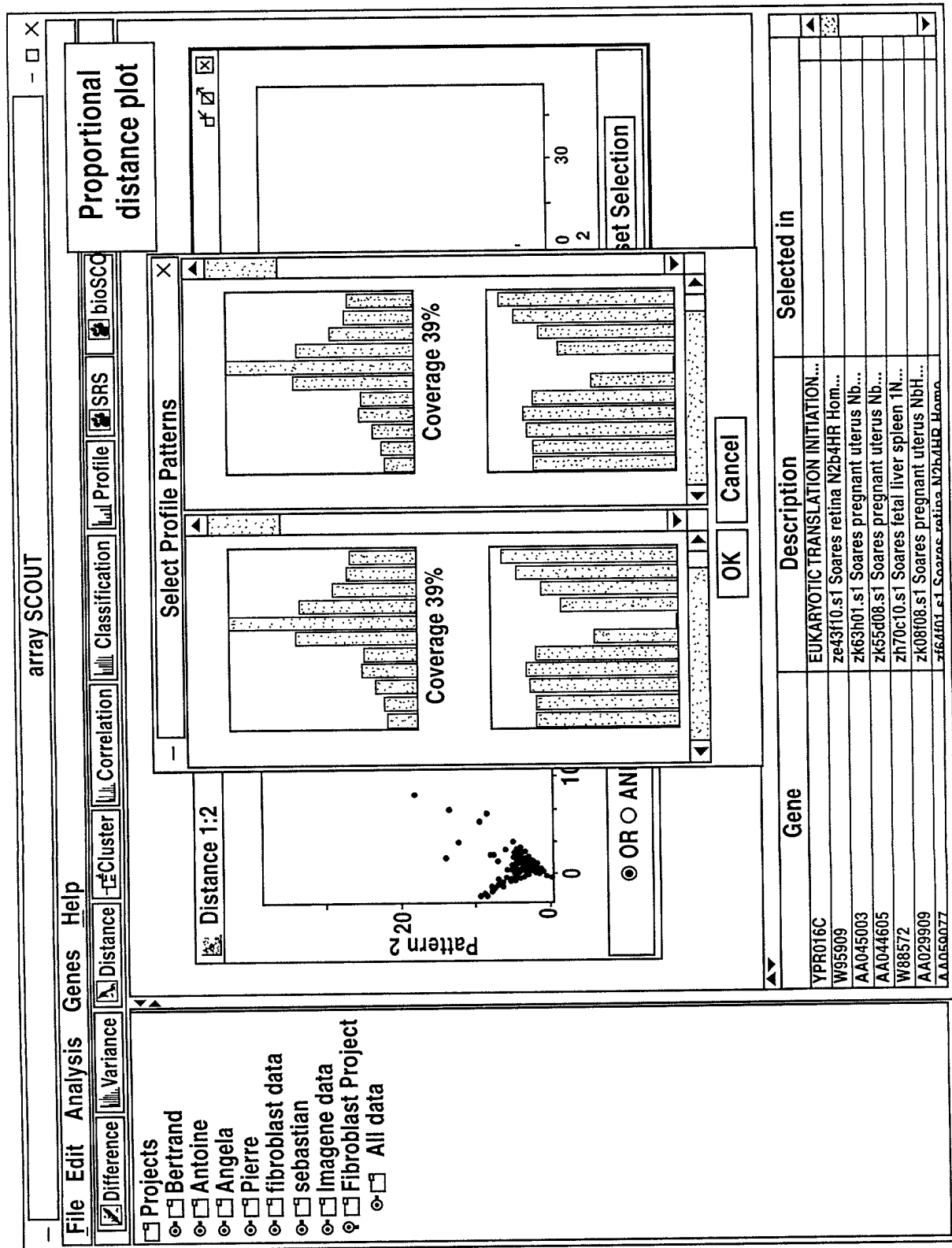


FIG.73

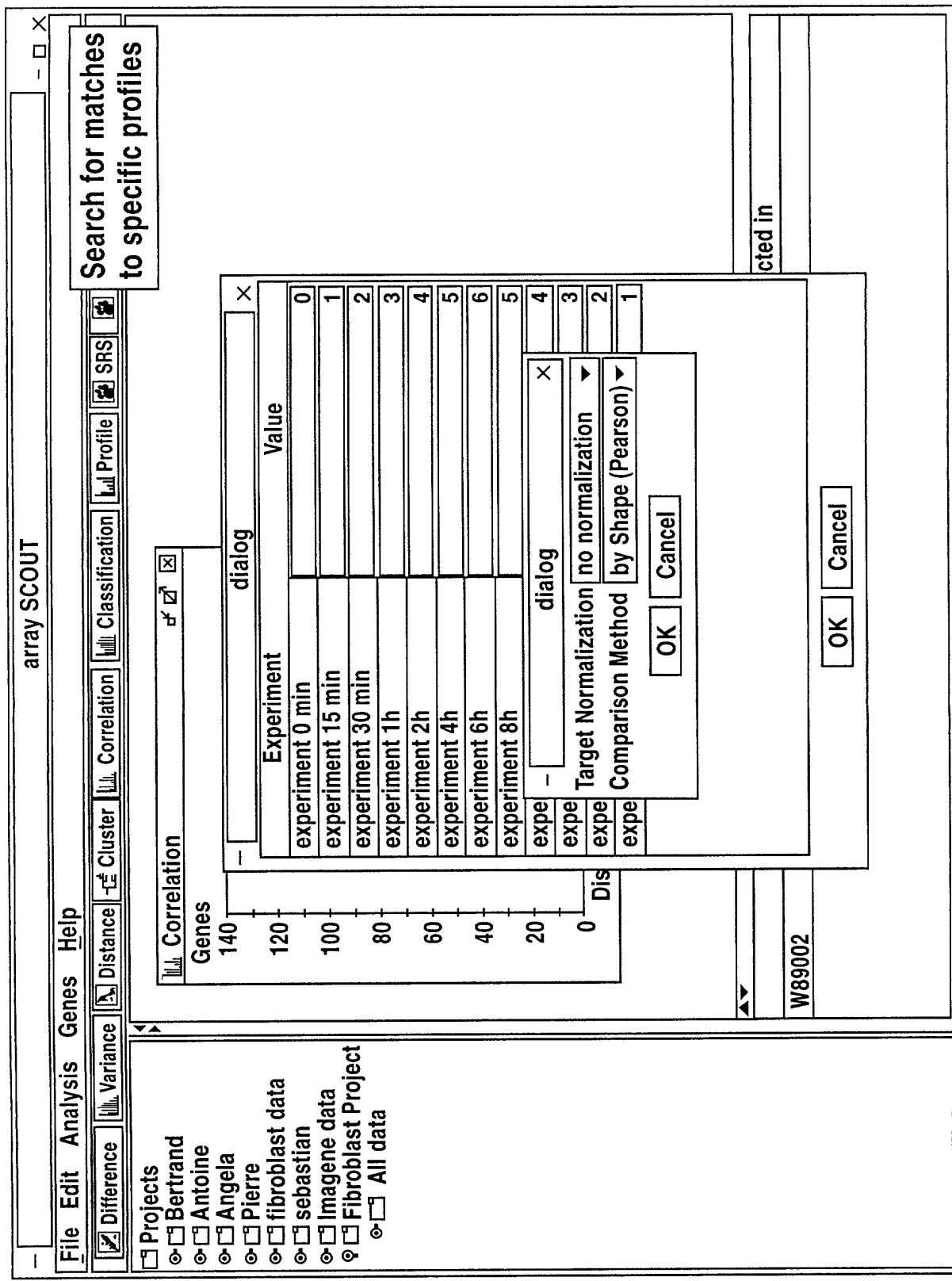


FIG.74

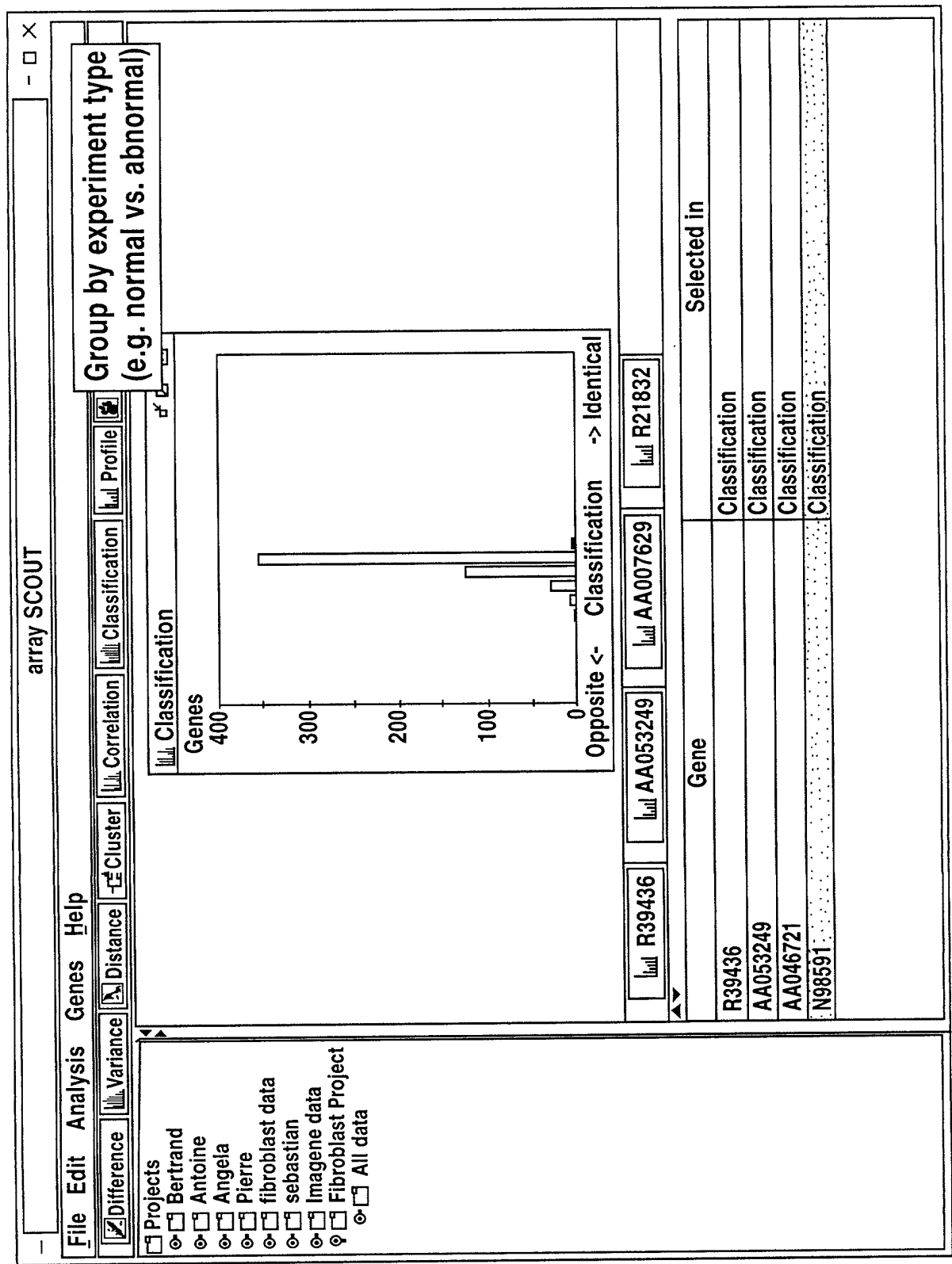


FIG. 75

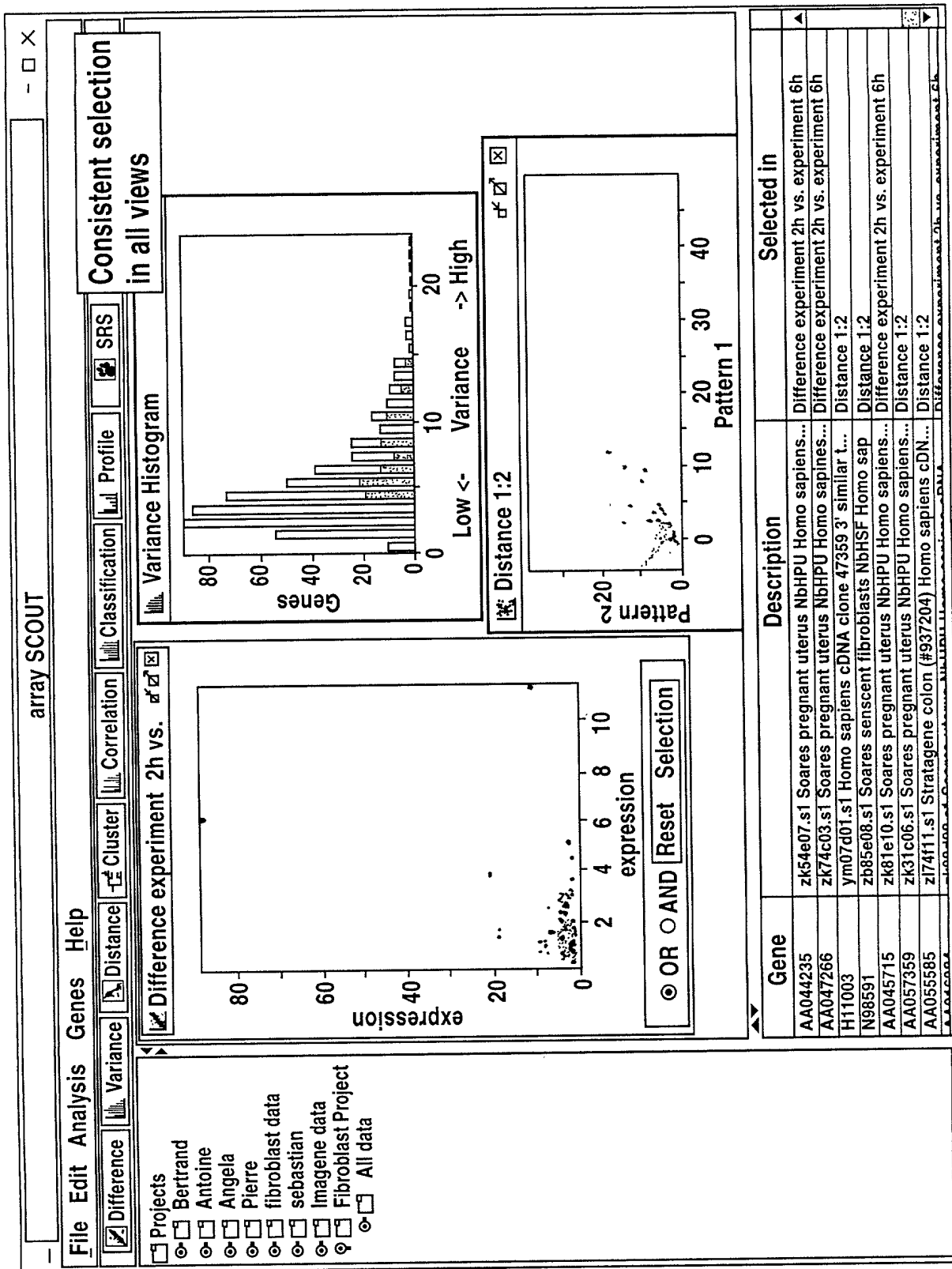


FIG.76

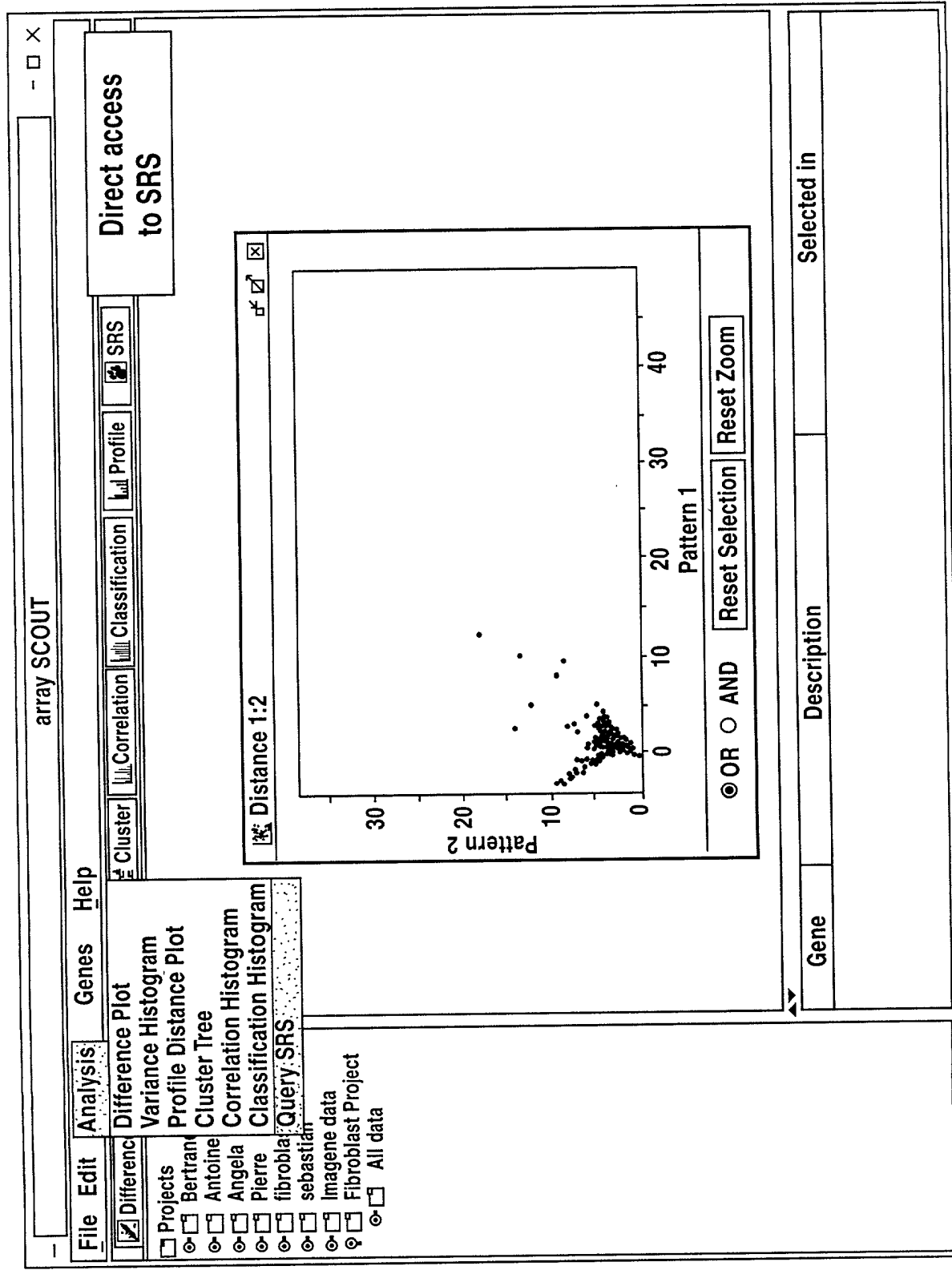
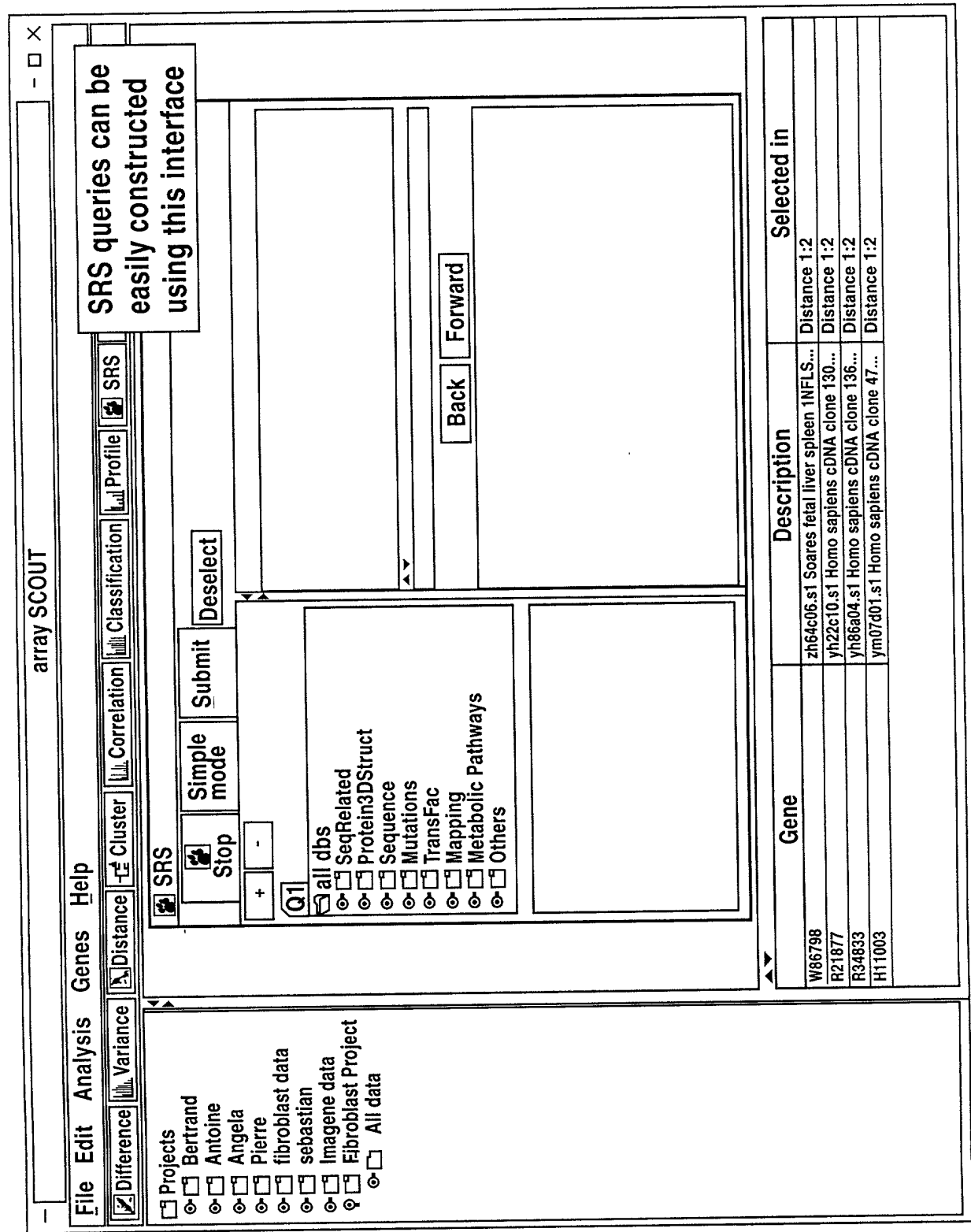


FIG.77



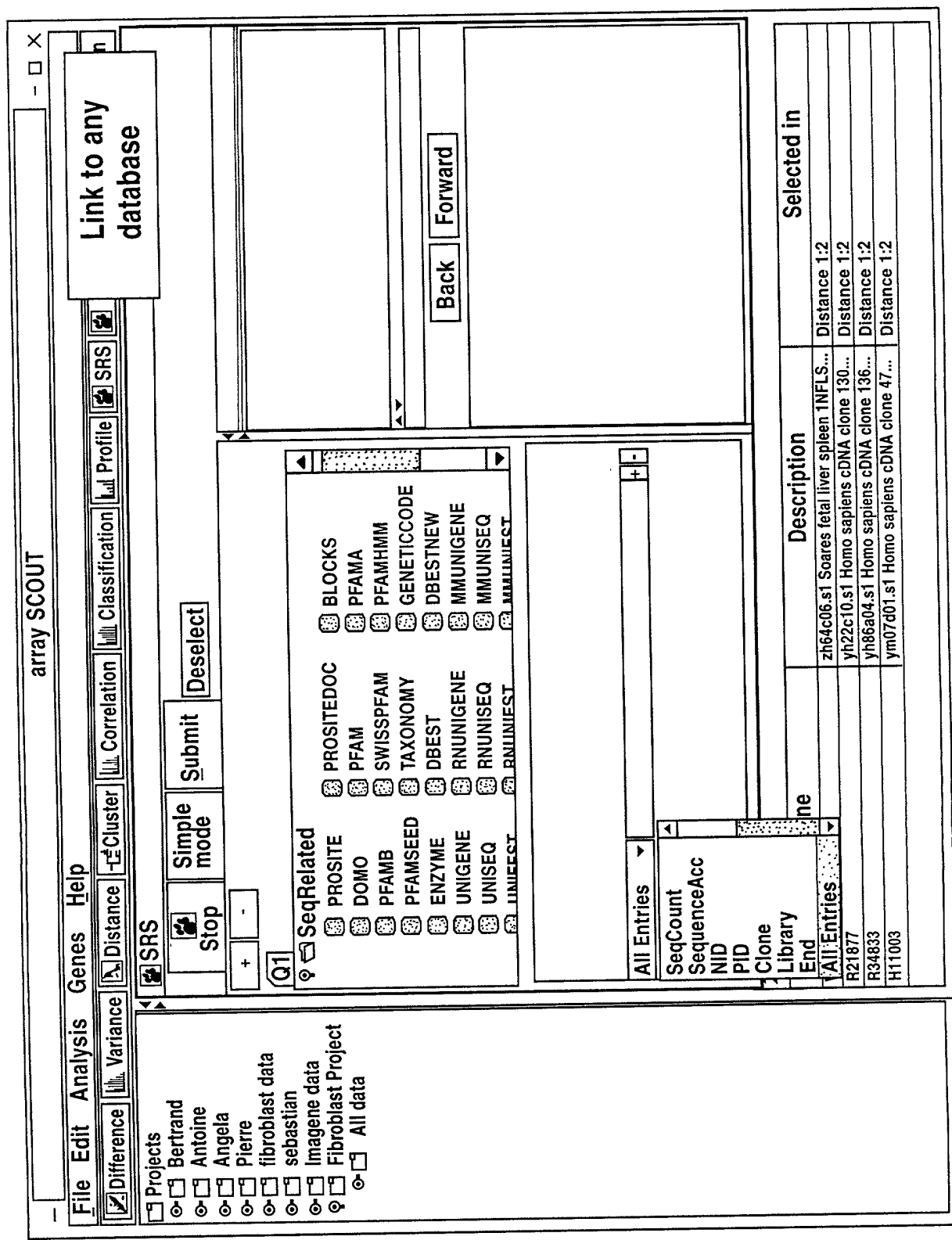
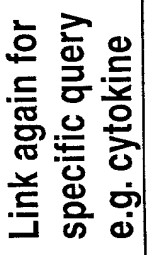


FIG.78



✕
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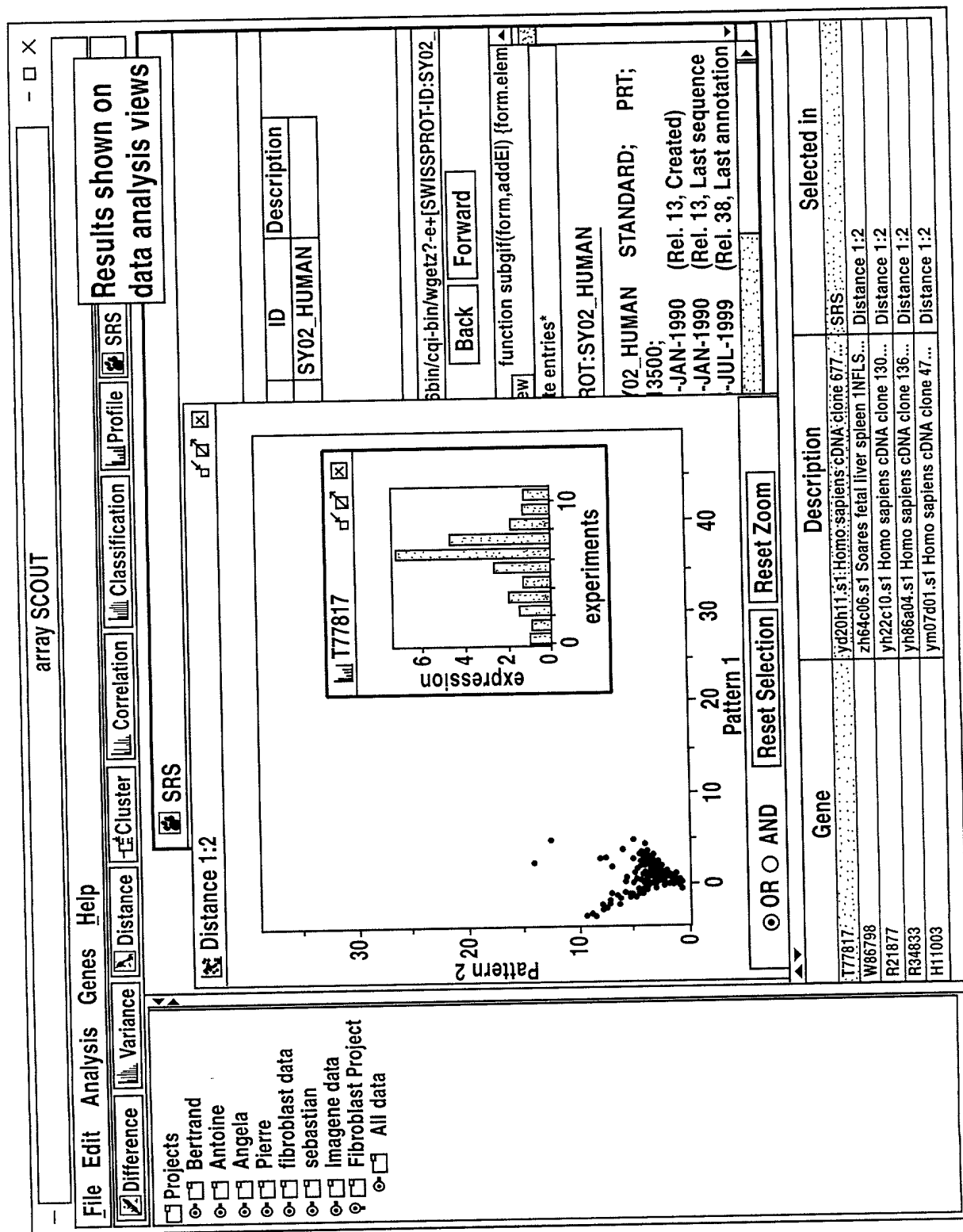


FIG. 81

FIG. 82

FIG.83

